of

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RESULT 15
I47160
Ig gamma 2b
C; Species:
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J. Immunol. 153, 3565-3573, 1994
A;Title: Five putative subclasses of swine IgG identified from A;Reference number: 147158; MUID:95015845; PMID:7930579
A;Accession: I47159
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma 2a chain constant region - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C;Accession: 14715
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C;Genetics:
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A; Residues: 1-328 <KAC>
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Sus scrofa
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                                                                                       RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
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SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                                                                                                              MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPPVLDSDGSFFLYSKLTVDKS 442
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                                                                                                                                                LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPPQQDVDGTYFLYSKFSVDKA
                                                                                                                                                                                                           STYRVYSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE
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constant region - pig (fragment)
rofa domestica (domestic pig)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1267; DB 2;
Pred. No. 1.6e-66;
2; Mismatches 52;
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C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #te C;Accession: I47160 R;Kacskovics, I; Sun, J; Butler, J.E. J. Immunol. 153, 3565-3573, 1994 A;Title: Five putative subclasses of swine IgG identif A;Reference number: I47158; MUID:95015845; PMID:793057 A;Accession: I47160 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-328 <KAC' A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA C;Genetics:
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C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:133-202/Domain: immunoglobulin homology <IMM>
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RWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
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SWQGGGIFQCAVMHEALHNHYTQKSISKTPGK 328
                                                                            MTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTPFVLDSDGSFFLYSKLTVDKS 442
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LSRSKVSITCLVIGFYPPDIDVEWQRNGQPEPEGNYRTTPFQQDVDGTYFLYSKFSVDKA 296
                                                                                                                                                                                    STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREE 384
                                                                                                                                                                                                                                                                   PSVFLEPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY/DGVEVHNAKTKPREEQYN 324
                                                                                                                                                                                                                                                                                                                            GLYSLSSMVTVPASSLSSKSYTCNVNHPATTTKVDKRVGTK/KRPPCPICPACESP----G 116
                                                                                                                                                                                                                                                                                                                                                    GLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPK;3CDKTHTCPPCPAPELLGG
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                                                                                                                                                                                                                                              PSVFIFPPKPKDTLMISRTPQVTCVVVDVSQENPEVQFSWYVDGVEVHTAQTRPKEEQFN 176
                                                                                                                                                                 STYRVVSVLPIQHQDWLNGKEFKCKVNNKDLPAPITRIISKAKGQTREPQVYTLPPHAEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50.2%; Score 1261; DB 2; 69.6%; Pred. No. 3.5e-66;
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Search completed: September 12, 2003, 13:04:25 Job time: 37.4831 secs

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A; Note: the sequence was determined from the germline gene R; Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R. Science 206, 1299-1303, 1979

A; Title: Structure of the constant and 3' untranslated region A; Reference number: A26235; MUID:80081501; PMID:117548

A; Contents: MPC 11

A; Accession: A26235

A; Molecule type: mRNA

A; Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU:
A; Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, Science 206, 1303-1306, 1979

A; Title: Sequence of the cloned gene for the constant region A; Reference number: A26232; MUID:80081502; PMID:117549

A; Accession: A26232

A; Molecule type: DNA

A; Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU:
R; Ollo, R.: Rougeon, F.
                                                                                                                                                                                                                                                     A;Introns: 138/1; 236/1; 258/1; 368/1
A;Introns: 138/1; 236/1; 258/1; 368/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap c;Complex: An immunoglobulin has IgA and IgM, the subunits associate into la C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin; 157-222/Domain: immunoglobulin homology <IM1>
F;336-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Molecule type: DNA
A:Residues: 138-161,'L',163-189,'FP',193-300,'R',302-331,'A',333-437,'DI',440-474
A:Residues: GB:J00461
A:Cross-references: GB:J00461
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Ta
J. Biol. Chem. 269, 12345-12350, 1994
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A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
A:Cross-references: EMBL:X67210; NID:g54826; PIDN:CAA47649.1; PID:g54827
A:Takabashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Accession: A02157
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R; Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
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A;Residues: 138-161,'L',163-189,'FP',193-474
A;Cross-references: GB:J00461
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Best Local
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MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                       MEWSWIFLFLLSGTAGVHSEVQLQQSGPELVNPGASVKMSCKASGYTFITYVMHWVKQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence is shown
                                                                                                                                                                                         55.5%;
                                                                                                                                                                   Score 1417; DB 1;
Pred. No. 4.8e-75;
6; Mismatches 124;
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A;Cross-references: EMBL:X13188; NID:g51780; PIDN:CAA31580.1; PID:g51781
A;NOte: this sequence was determined from the differentiated gene
C;Superfamilly: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Expression A; Reference number: A; Accession: S01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fier Eur. J. Biochem. 176, 287-295, 1988
A;Title: Expression in non-lymphold cells of mouse recombinant A;Reference number: S01320; MUID:88329081; PMID:3138116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig gamma-2b chain precursor - mouse C; Species: Mus musculus (house mouse) C; Date: 30-Sep-1989 #sequence_revision C; Accession: S01321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;20-475/Product: F;159-223/Domain:
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A; Residues: 1-475 <DE1>
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Best Local S
Matches 266
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;20-475/Product: Ig gamma-2b chain #status predicted
;159-223/Domain: immunoglobulin homology <IMM>
241
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                                                                                                                                                                                                                                                                                                                                             MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
RVEPKSCDKT-HTCPP-----CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDV
                                                                     VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                                               VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP 180
                                                                                                                                                                                                                               GQGLEWIGEIYPGSGNSYFNEKFKGKATLTVDKSSSTAYLHLSSLTSEDSAVYFCAGPRQ
                                                                                                                                                                                                                                                                                                                       MEWIWIFLFILSGTAGVQSQVQLQQSGAELARPGASVKLSCKASGYTLTSYGISWVKQRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                             VTVTWNSGSLSSSVHTFPALLQ-SGLYTMSSSVTVPSSTWPSQTVTCSVAHPASSTTVDK
                                                                                                                                       VGLL----PFGYWGQGTLVTASAAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TEENYKDTAPVLDSDGSYFIYSKLNMKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
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                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 1401.5; 55.3%; Pred. No. 3.8
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                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 3.8e
2; Mismatches
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3.8e-74;
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R.Khamlichi, A.A.
submitted to the EMBL Data Library, September A:Reference number: $72664
                                                          RESULT
S40295
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If heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Blochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
Ig gamma-2a chain (mAb735) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Apr-1994 #sequence_revision
C;Accession: S40295
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A;Residues: 1-140, C',142-374 <KH2>
A:Cross references: EMBL.X81695
C:Superfamily: immunoglobulin C reg
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A; Residues: 1-374 <KHA>
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                                                                                                                  GK
                                                                                                                                              GK 474
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                                                                                                                                                                                                                                                                                                       VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GYGQGYRFHSWGQGTLVTVSS----
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          07-Apr-1994 #text_change 16-Jul-1999
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nes 54;
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RESULT 12 G2MS11

If gamma-2b chain - mouse (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000 C;Date: 31-Mar-1980 #sequence_revision R26232; A26233; A33598 R;Fischer: R: Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzalk submitted to the EMBL Data Library, July 1992 A;Description: Production of a Tobacco mosaic virus (TMV) inactivating neoto

A; Reference number: A; Accession: S25057

S25057

inactivating neotop

specifi

H.J.; Kreuzaler,

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R;Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Submitted to the EMBL Data Library, January 1993
A;Description: Primary structure of the murine monoclonil IgG2a ant A;Reference number: $40295
A;Accession: $40295
A;Molecule type: protein
A;Residues: 1-446 <KLE>
C;GenetLcs:
A;Map position: 12
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Reywords: disulfide bond; glycoprotein; immunoglobulin; pyrogluta
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;1-117/Domain: V-D-J region <VDJ>
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F;118-214/Domain: C region <CCHP>
F;118-214/Domain: C1 region <CCHP>
F;118-214/Domain: C2 region <CCHP>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CCH2>
F;341-446/Domain: C3 region <CCH3>
F;340-427/Domain: immunoglobulin homology <IMM>
F;160-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;322/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
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Best Local
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                                                                           LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN::KTTPPVLDSDGSFFLYSKL
                                                                                                                                                             THREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKDLPAPIERTISKPKGSVRAPQVYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAFGKGLEWVSAISASGHSTYL
RVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTPG
                                                                                                                                                                                                                                           VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEFVTVSWNSGALTSGVHTFPA 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QIQLQQSGPELVRPGASVKISCKASGYTFTDYYIHWVKQRFGEGLEWIGWIYPGSGNTKY
                                      TVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                   PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAI·IEKTISKAKGQPREPQVYT 377
                                                                                                                                                                                                                                                                                                                               VLQSD-LYTLSSSTVTSSTWPSQSITCNVAHPASSTKVDI:KIEPRG-PTIKPCPPCKCP
                                                                                                                                                                                                                                                                                                                                                       VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDLRVEPKSCDKTHTCPP--CP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEKFKGKATLTVDTSSSTAYMQLSSLTSEDSAVYFCARGGFFAM------DYWGQGTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADSVKGRFTISRDNSKNTLYLOMNSLRAEDTAVYYCAKDREVTMIVVLNGGFDYWGQGTR 139
                                                                                                                                                                                                                                                                                                                                                                                                               VTVSSAKTTAPSVYPLAPVCGDTTGSSVTLGCLVKGYFPEIVTLTWNSGSLSSGVHTFPA
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                                         473
446
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418

293 358 353

413

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S37483
S37483
Ig gamma-2a chain -
C:Species: Mus musc
C:Date: 06-Jan-1995
C:Accession: S37483
R:Ducancel, F.F.D
                                                                                                                                                                                                                                            submitted to the EMBL Data Library, February 1993
A; Reference number: $37483
A; Accession: $37483
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-469 < LOUC>
A; Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C; Superfamily: immunoglobulin C region; immunoglobulin C:Keywords: immunoglobulin C:Keywords: immunoglobulin C:Keywords: immunoglobulin homology
F; 276-345/Domain: Immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                             g gamma-2a chain - mouse
;Species: Mus musculus (house mouse)
;Date: 06-Jan-1995 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                      Accession: S37483
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hes 281;
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VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                       LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSFGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGGF-DYWGQGTRYTYSSASTKGPSYFPLAPSSKSTSGGTAALGCLYKDYFDEPYTYSWN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTTPPV 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DDVEVNTATTKPREEQFNSTYRVVSALRIQHQDWTGGKEFKCKVHNEGLPAPIVRTISRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGAIADAWGQGLLVTVSSASTTAPKVYPLSSCCGDKSSSTVTLGCLVSSYMPEPVTVTWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGIT-SGGTTYYNPALKSRLSITKENSKSQVSLSVSSVTPEDTATYYCARS---TYGEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVL 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDADSSYFLYSKLRVDRNSWQEGDTYTCVVMHEALHNHYTQKSTSKSAGK 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKS 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LFVLSAPIGVLSQVQLRESGPSLVKPSQTLSLTCTVSGFSLSSYALTWVRQAPGKALEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KGPAREPQVYVLAPPQEELSKSTVSLTCMVTSFYPDYIAVEWQRNGQPESEDKYGTTPPQ
                                                                                                                                                                                             Conservative
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62.1%;
                                                                                                                                                                                             78;
                                                                                                                                                                                                      Score 1482.5; DB Pred. No. 7.6e-79;
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Pred. No. 9.6e-80;
1; Mismatches 107;
                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                             104;
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                                                                                                                                                                                                                   Length 469;
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$31459
Ig gamma-1 chain - sheep (fragment)
C; Species: Ovis orientalis aries, Ovis amu
C; Date: 13-Jan-1995 #sequence_revision 13
C; Accession: $31459
R; Patri, S.; Nau, F.
submitted to the EMBL Data Library, Decer
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C;Superfamily: immunoglobulin C r
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin
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A; Residues: 1-472 <PAT>
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                                                                                                                                                                                                                                                                                                                                                                     RVEPKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDP
                           TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTSQLDADGSYFLYSRLRVDKNSWQEGDTYACVVMHEALHNHYTQKSISKPPGK
                                                                             ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKT
                                                                                                               SWFYDNYEYRTARTKPREEQFNSTFRYVSALPIQHQDWTGGKEFKCKVHNEALPAPIVRT
                                                                                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                             EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                     SHAFAYASYDFWGPGLLISVLSASTTPPKVYPLTSCCGDTSSSIVTLGCLVSSYMPEPVT
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                                                                                                                                                                 EPGCPDPCKHC-RCPPPELPGGPSVFIFPPKPKDTLTISGTPEVTCVVVDVGQDDPEVQF
                                                                ISRTKGQAREPQVYVLAPPQEELSKSTLSVTCLVTGFYPDYIAVEWQKNGQPESEDKYGT
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                    58.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1455; DB Pred. No. 3e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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13-Jan-1995
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358

242

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A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14932.33-14632.33

A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical ligh hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate in c;Superfamily: immunoglobulin c region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin fr;20-85/Domain: immunoglobulin homology <IM1>
F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>
F;240-307/Domain: immunoglobulin homology <IM3>
F;140/Disulfide bonds: interchain (to light chain) #status experimental F;27-83,141-201.247-305/Disulfide bonds: #status predicted
F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Molecule type: DMA
A;Residues: 1-327 <ELL>
A;Note: the sequence was determined from the R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.
Biochem. J. 117, 33-47, 1970
A;Title: Human immunoglobulin sublclasses. Pa A;Reference number: A90249; MUID:70207560; PMA;Accession: A90249
                                                                                                                           RESULT 6
PC4436

MCDACCESSION: PC4436

R; Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.
Blochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 agair A; Reference number: JC5810; MUID:98063277; PMID:9398605

A;Accession: PC4436
   A; Molecule type: protein
A; Residues: 1.444 < AKKA>
C; Comment: This catalytic antibody has processed in the comment of the catalytic antibody has processed in the comment of the commen
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Pred. No. 8.4e
9; Mismatches
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; immunoglobulin
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A; Molecule type: DNA
A; Residues: 142-470 <SYM>
A; Residues: 142-470 <SYM>
A; Cross-references: EMBL: X16701
A; Note: the sequence was determined from the germl C; Genetics:
A; Gene: Ig CH gamma-1
A; Introns: 98/1; 111/1; 221/1
C; Superfamily: immunoglobulin C region; immunoglob C; Keywords: glycoprotein; heterotetramer; immunogl F; 161-225/Domain: immunoglobulin homology <IMM>
F; 318/Binding site: carbohydrate (Asn) (covalent)
                                                                                                                                                                                                                                                                                                                                                                 R;Sanders, P.G.
submitted to the EMBL Data
submitted to umber: S22080
                                                                                                                                                                                           A;Cross-references: EMBL:X62916; NID:g439; F R;Symons, D.B.A.; Clarkson, C.A.; Beale, D. Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin A;Reference number: S06610; MUID:90097956; P A;Accession: S06610
                                                                                                                                                                                                                                                                                                                                                                                                                       Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine R;Alternate names: Ig gamma-1 chain C region (clone C:Species: Bos primigenius taurus (cattle) C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #c;Accession: S22080; S06610; A31303
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A; Residues: 1-470 <SAN>
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PAVLQSD-LYTLSSSYTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDCG----CKPCI
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Pred. No. 1.8
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RESULT 4

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ALHNRFTQKSLSLSPGK 377
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Pred. No. 6.2e-88,
7; Mismatches 1:
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RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence_revision 02-Apr
C:Accession: A90933; A90249; A02150
R:Ellison, J:; Buxbaum, J:; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immun
A:Reference number: A90933; MUID:83157104; PM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83.140-200.246-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Map position: 14q32.33-14q32.33

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <AINT: 133-202 | Armonoglobulin homology <AINT: 133-202 | Armon
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A;Title: Disulphide bridges of the heavy chain of human A;Reference number: A90253; MUID:72033500; PMID:4940472
A;Contents: annotation; myeloma protein Sa, disulfide bo R;Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
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A;Residues: 238-275 <HOS>
A;Residues: 7.; Parr, D.M.
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March
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C; Genetics:
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A; Contents: annotation; Zie,
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02-Apr-1982

#text_change

16-Jul-1999

immunoglobulin 04; PMID:6299662

C-gamma4

gene

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A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 1432.33-14432.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la C;Complex: An immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F;20-85/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83,144-204,250-308/Disulfide bonds: #status experimental
F;109,112/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;109,112/Disulfide carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Molecule type: protein
A; Residues: 1-96, 'R', '98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330
A; Note: this sequence has the Glm(3) and Glm(non-1) markers
R; Gall, W.E.; Edelman, G.M.
Blochemistry 9, 3188-3196, 1970
A; Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disu
A; Reference number: A90565; MUID:71064027; PMID:4923144
A; Reference number: A90565; MUID:71064027; PMID:4923144
A; Contents: annotation; disulfide bonds
R; Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Dhysiol. Chem. 357, 1515-1540, 1976
A; Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immuno enbromide cleavage products, and the disulfide bridges.
A; Reference number: A91667; MUID:77070267; PMID:1002129
A; Contents: annotation; disulfide bonds
C:Genetics:
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A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',A;Residues: 1-34,'Q',36-96,'K',98-115,'Q',117-197,'D',199-238,'D',240,'L',242-268,'E',A;Rote: thits sequence has the Glm(17) and Glm(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Prinaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 1
A;Reference number: A91723; MUID:83289131; PMID:6884994
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A; Reference number: A91668;
A; Contents: myeloma protein
A; Accession: B91668
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                                                                                                                                                                                                                                                                                                            PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN
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                                                                                                                                                                                                        STYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE
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99.1%;
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Pred. No. 5.5e-95;
3; Mismatches 0;
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A; Molecule type: DNA
A; Residues: 1-377 (HUC)
A; Residues: 1-377 (HUC)
C; Superfamily: immunoglobulin
C; Keywords: immunoglobulin
F; 20-85/Domain: immunoglobulin
                                                                                                R;Huck, S.; Lefranc, G.; Lefranc, M.P.
Immunogenetics 30, 250-257, 1989
A;Title: A human immunoglobulin IGHG3 allele
A;Reference number: A60764; MUID:90007613; PM
A;Accession: A60764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, Nucleic Acids Res. 14, 1779-1789, 1986
A;Title: Sequence of a human immunoglobulin gamma 3 heavy cha A;Reference number: A23511; MUID:86148507; PMID:3081877
A;Accession: A23511
A;Molecule type: DNA
A;Residues: 1-377 <HUC>
A;Cross-references: GB:X03604; GB:M12958; NID:g33070; PIDN:CA
                                                                                                                                                                                Ig gamma-3 chain C region, form LAT - 1
C;Species: Homo sapiens (man)
C;Date: 14-May-1993 #sequence_revision
C;Accession: A60764
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A;Map position: 14q32.33-14q32.33
A;Introns: 98/3; 115/3; 130/3; 145/3; 16
C;Superfamily: immunoglobulin C region; C;Keywords: immunoglobulin bomology
F;20-85/Domain: immunoglobulin homology
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                                                                                   A;Status: preliminary
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A;Gene: GDB:IGHG3
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|||| :|| ||| ||| || || || || || ALHNRFTQKSLSLSPGK 377
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                                  C region; immunoglobulin
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Pred. No. 4.7e
7; Mismatches
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conv

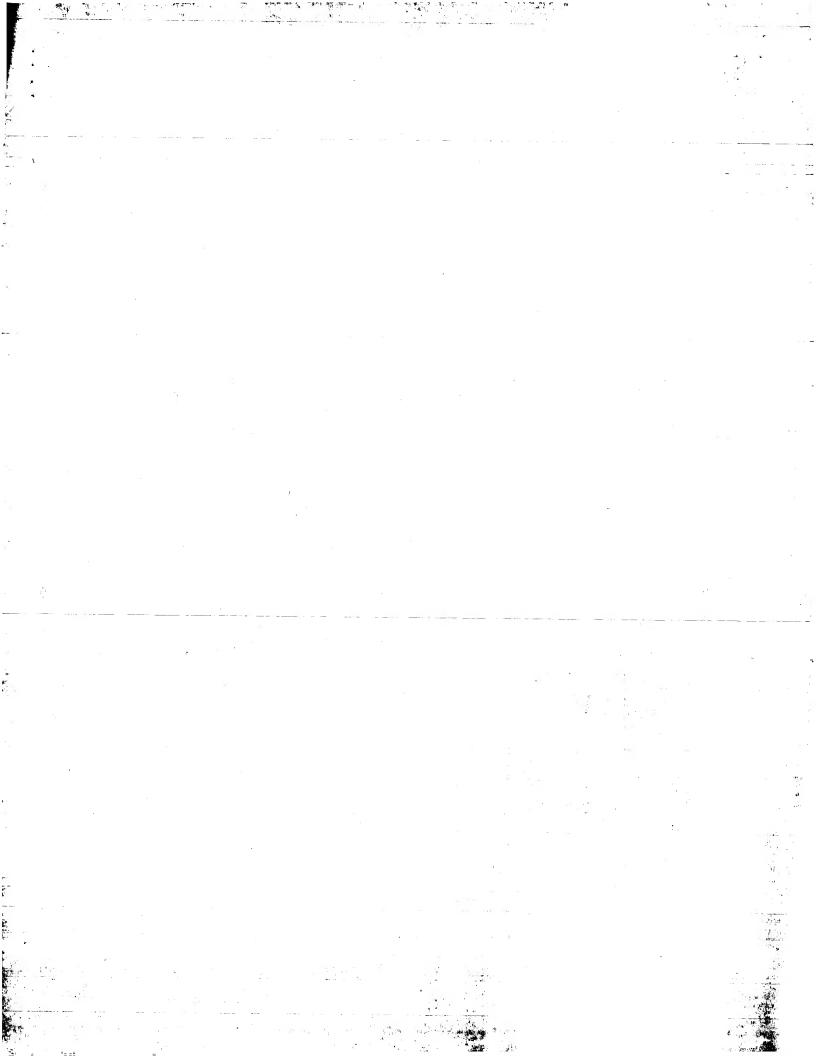
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Title:
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Maximum Match 10
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45	44	43	42	41	40	39	38	37	36	ω 5	34	ω	32	31	30
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31.5	31.5	32.9	33.7	34.5	35.0	39.9	42.6	43.0	43.5	44.3	44.4	44.7	44.8	44.8	44.9
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Ig mu chain precur	Ig heavy chain (DO	Ig gamma-1 heavy c	Ig heavy chain V-I	Ig heavy chain pre	Ig Y heavy chain (Ig heavy chain VHI	Ig gamma 4 chain c	Ig gamma-2b chain	Ig gamma-2 chain C	Ig epsilon chain C	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2a chain	Ig gamma-2c chain	Ig gamma-2a chain

ALIGNMENTS

RESULT 1
GHHU
Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90584; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gammal gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Residues: 1-340 <ELL>
A;Residue

אייזורופ: הופ אבושקפנצנות etues monokionaten iger. יוווווווון להאפרטוווווע (אאפרטווווע אייזורופ: אייזורופי איי	19 gamma-3 chain C
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976	Ig gamma-1 chain C
R; Ponstingl, H.; Hilschmann, N.	
A; Note: this sequence has the Glm(non-1) markers, 239-Glu and 241-Met	
A; Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2	
A; Molecule type: protein	Ig gamma-1 chain C
A;Accession: A90564	Ig gamma-3 heavy c
A;Contents: Eu	Ig heavy chain C r
A; Reference number: A90564; MUID:71064025; PMID:5530842	
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se	Ig gamma 3 chain c
Biochemistry 9, 3171-3181, 1970	Ig gamma chain C r
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.	Ig gamma 1 chain c
	Ig gamma chain C r
A; Residues: 1-96, 'R', 98-135 < CUN>	
A; Molecule type: protein	Ig gamma 2b chain
A;Accession: B90563	
A;Contents: myeloma protein Eu	Ig gamma-2b chain
A; Reference number: A90563; MUID:71064024; PMID:5489771	
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq	Ig gamma-2a chain
Biochemistry 9, 3161-3170, 1970	Ig heavy chain V r
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelma	Ig gamma-1 chain -
	Ig gamma-2a chain
A; Residues: 88-113;235-330 <tak></tak>	Ig heavy chain pre
A; Molecule type: DNA	monoclonal antibod
A; Accession: S33887	Ig gamma-4 chain C
A; Reference number: S33887; MUID:83001943; PMID:6811139	Ig gamma-2 chain C
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of	Ig gamma-3 chain C
Cell 29, 671-679, 1982	Ig gamma-3 chain C
R; Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.	Ig gamma-1 chain C
A;Cross-references: EMBL:Z17370	
A; Residues: 2-330 <har></har>	Description
A; Molecule type: DNA	
A; Accession: S36861	
A;Reference number: S33904	
submitted to the EMBL Data Library, October 1992	
R;Harris, L.J.	stribution.
	result being printed,
A; Note: this sequence has the Glm(17) allotypic marker, 97-Lys, and the Glm(1) marker	chance to have a
A;Cross-references: EMBL:217370	
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RESULT 15
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New humanized forms of mouse 3D6 antibodies, useful for treating Down's syndrome, (pre-)clinical Alzheimer's disease or (pre-)clinical cerebral amyloid angiopathy, or for inhibiting formation of or reducing Abeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Monoclonal antibody; 3D6; complementarity determining region; CD mouse; human; humanised antibody; antibody; Alzheimer's disease; Down's syndrome; cerebral amyloid angiopathy; neuroprotective;
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                                 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                               EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP 379
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DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                               ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, is also useful for treating osteopenic disorder, an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a patient or rheumatoid arthritis in a patient. In particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis, paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antibodies that interact with osteoprotegerin ligands, useful for treating osteopenic disorders, e.g. osteoporosis, bone loss from arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and osteonecrosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, wenkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Fig
   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                       Sequence
                                           25-MAR-2003
28-DEC-1992
                                                                            AAR24812;
                                                                                               AAR24812 standard; Protein; 466
                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                 238
                                                                                                                                                                                                                                                                                                     241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                  TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSBGK 474
                                                                                                                                                                                                                                                                                                                         TTVIM----SWFDPWGQGTLVTVSSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                                                                              GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE 120
                                                                                                                                                                                                       KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                      QFNWYVDGVEVHNAKTKPREEQFNSTFRVVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIE
                                                                                                                                                                                                                                                KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                                               MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                       encoded by the chimeric H chain cDNA contained in
                                                                                                                                                                                            KTISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                            GKGLEWVSGITGSGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                          (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; 144pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2244.5; DB 24; Length Pred. No. 2.3e-132;
anti-fibrin antibody; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      467
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                      ртв1373
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chimeric anti-human firbrin heavy chain cDNA open reading
cframe. It was prepd. using Poly(A)+ RNA from the anti-fibrin
cc chimeric Ab-producing transformant FIBI-HOLYAG as a template
cc to clone human C-kappa cDNA, using the oligo-dT (Fharmacia) primer as
ca primer for first strand cDNA synthesis and the 5'C2H and 3'EH
cprimers for the PCR. A human gamma-1 chain CH2-CH2 domaine encoding
cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
ce encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
cpeptide cDNA were amplified using the primers 3'EH; 3'C2H and 3'CH
crespectively as a primer for first strand cDNA synthesis and the
cprimer combination of 5'C1H and 3'C2H, of 5'LH and 3'C1H and of
cyrimer combination of 5'C1H and 3'C2H, of 5'LH and 3'C1H and of
cproducts were isolated and used to produce plasmids. After
confirmation of the cDNA sequence of each plasmid, the cDNA
cencoding LH, VH, CH1 and CH2CH3 were joined toge!:her to give
confirmation of the cDNA sequence of each plasmid, the cDNA
cplasmid pTB1373 contg. the whole length chimeric II chain
(LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIII,
  Query Match
Best Local S
Matches 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric monoclonal antibodies - contain anti-human fibrin antibody light and heavy chain variable and constant for treating thrombotic conditions e.g. myocardial infarction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1990;
11-NOV-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP491351-A2
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                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Figure 11; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Iwasa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-DEC-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 - JUN - 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pTB1373 contains the whole length of a mouse-human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Taka
                                                                                               466
  Conservative
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91JP-0294464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers 13..19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248..357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "translated stop codon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CH3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= CH2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= hinge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= VH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Leader
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..232
..232
... CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 247
                      89.3%;
  18;
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Score 2244; DB 13;
Pred. No. 2.5e-132;
8; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tada
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     Indels
                                               Length
                                                  466;
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                                                                                                                                                                                                                            mediated immunological or inflammatory disorders such as skin related Conditions (e.g. psoriasis, eczema, burns, dermatitis and abnormal Condiferation of hair follicle cells), fibrosis (e.g. kidney or lung Cfibrosis), allergic rinhitis, respiratory distress syndrome, asthma, conditis, tendonitis, bursitis, fever, migraine headaches, gastro-conchitis, tendonitis, bursitis, fever, migraine headaches, gastro-conchitis, irritable bowel syndrome, colitis and colorectal cancer), vascular diseases (e.g. atherosclerosis), thyroiditis, aplastic anaemia, periarteritis nodosa, Hodgkin's disease, rheumatic fever, osteoarthritis, periartic systemic lupus erythematosus and multiple sclerosis), renal carthritis, systemic lupus erythematosus and multiple sclerosis), renal carthritis, systemic lupus erythematosus and multiple sclerosis, renal colorectis, hypersensitivity (e.g. delayed type hypersensitivity or immediate hypersensitivity), graft and transplant rejections, graft
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; very late activation antigen; VLA-1; betal containing integrin; Immunological disorder; inflammatory disorder; skin related condition; psoriasis; eczema; burn; dermatitis; respiratory distress syndrome; fibrosis; allergic rhinitis; asthma; bronchitis; tendonitis; bristitis; fever; migraine headache; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; colitis; colorectal cancer; vascular disease; atherosclerosis; thyroiditis; aplastic anaemia; periarteritis nodosa; gastritis; Hodgkin's disease; rheumatic fever; autoimmune disease; osteoarthritis; type I diabetes; myasthenia gravis; rheumatoid arthritis; systemic lupus erythematosus; multiple sclerosis; nephrotic syndrome; renal failure; sarcoidosis; Behoet's syndrome; gingivitis; polymyositis; hypersensitivity; graft rejection; transplant rejection; conjunctivitis; graft versus host disease; myocardial ischaemia.
                                                                                           Sequence
                                                                                                                                             versus host disease, conjunctivitis, swelling occumyocardial ischaemia or endotoxin shock syndrome. is human AQC2 heavy chain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel antibodies that specifically bind to very late activation (VLA-1; betal containing integrins) antigens and methods of using these antibodies to treat immunological disorders. The antibodies are useful for preventing or treating VLA-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New anti-VLA-1 antibodies are useful for preventing or treating VLA-1-mediated immunological or inflammatory disorders, e.g. psoriasis, eczema, burns, dermatitis, and abnormal proliferation of hair follicle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-APR-2001; 2001US-283794P
06-JUL-2001; 2001US-303689P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAE33522 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-APR-2002; 2002WO-US11521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Page 75; 248pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or fibrosis
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                                                                                              447
                                                                                           ĄΑ;
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   93
93
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. 3%;
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Score 2244.5; DB 2
Pred. No. 2.2e-132;
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                                                                                                                                                                          swelling occurring after injury, ock syndrome. The present sequence
                            24;
                            Length 447;
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RESULT 13
ABP71365
ID ABP71367
XX ABP71
XX ABP71
XX ABP71
XX ABP71
XX OStec
KW OStec
KW OStec
KW antia
XX Mus m
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WPI; 2003-210262/20
N-PSDB; ABZ59147.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osteoprotegerin ligand; osteopathic; antlinflammatory; antirheumatic; antlarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.
                                                                            Boyle WJ,
                                                                                                                             (ABGE-)
                                                                                                                                                                                                            26-JUN-2001; 2001US-301172P
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                                                                                                                                                                                                                                                           25-JUN-2002; 2002WO-US20181
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                                                                                                                             ABGENIX INC.
AMGEN INC.
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                                                                            Martin FH,
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/note= "variable region"
                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "IgG2 signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                            Corvalan
                                                                                                                                                                                                                                                                                                                                                                                                           "constant region"
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                                                                            JR,
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RESULT 11
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XX AAE34
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XX 28-M2
XX BIWA4
XX BIWA6
XX BIWA6
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Best Local Sim
Matches 423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequences (AAO54651-52) show the light and heavy chain cDNAs of murine T84.12. The T84.12 antibody is directed against the tumour marker carcinoma embryonic antigen, and is useful for tumour imaging and immunotherapy.

The amino acid sequence given in the specification has been incorrectly identified as a nucleic acid sequence, therefore unacceptable characters have been represented as an 'N'. The amino acid sequence given below has been derived from the cDNA, by the indexer.

(Updated on 25-MAR-2003 to correct PN field.)
                Unidentified
                                                                              28-MAY-2003
                                                                                                AAE34876
                                                                                                                 AAE34876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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igen - has
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                                 antibody;
L; CD44v6;
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                                                             antibody
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                                                                                                                                                                                                                                                                                                                                           VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP: --IDYYGGGGFGYWGQGTLATVSAASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                      TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                             KTISKAKGQPREPQYYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                          KFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                                                                                                                                                                                                                                                                     VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                                                                                                                                                                                                                                           MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                            TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                   KFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
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                                                                                                                                                                                                                                                                                                                                                                                                                   MNFGFSLIFLVLVLKGVQCEVKLVESGGGFVKPGGSLKLSCAASGFTFSSYAMSWVRQTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c T84.12 antibody active against carcinoembryonic
s murine variable and human constant regions, also
it and transformed myeloma cells
                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-23; 27pp; English.
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                                 heavy chain medicament;
                                                            heavy chain
                                                                                                                Protein;
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                                variable region; light chain cancer; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 2257; DB 15; Pred. No. 3.9e-133;
                                                            mature
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                                                                                                                 A
                                                            protein
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Query Match
Best Local S
Matches 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-2001;
26-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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DB; AAD53212, AJ
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BOEHRINGER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                             EVOLLESGGGLVOPGGSLRLSCAASGFTFSNYAMSWVRQA;GKGLEWVSAISASGHSTYL 79
                                                                                                                                                                                            VLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAPVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                                                                ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDR EVTMIVVLNGGEDYWGQGTR 139
                 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                               PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYI.TTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                LDSIKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARQ---
                                                                                                                                                EEQYNSTYRVYSVLTVLHQDWLNGKEYKCKVSNKALPAPJEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYDMSWVRQA?GKGLEWVSTISSGGSYTYY
                                                               PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYI:TTPPVLDSDGSFFLYSKLTV
                                                                                                                               EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAP) EKT I SKAKGQPREPQVYTLP
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2001US-325147P
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The invention describes an isolated mucin-1-specific binding member having an antigen binding domain including a region that comprises a specific amino acid sequence. The inventive MUC1-specific binding member is used in the diagnosis and/or treatment of cancer, e.g. adenocarcinoma, found in various tissues, e.g. breast, ovary, bladder, and lung. It can be used alone or as a component in a more complex anti-cancer regimen which may contain anti-cancer drug(s) and/or radiation treatment(s). The inventive binding member recognizes tumour-associated MUC1 on adenocarcinoma. Its affinity is high enough to bind to tumour cells. This is the amino acid sequence of a mucin 1 (MUC-1) specific antibody region used to isolate MUC-1 antigen binding domains for use in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mucin-1-specific binding member; human; cancer; adenocarcinoma; breast cancer; ovarian cancer; bladder cancer; lung cancer; anti-cancer regimen; anti-cancer drug; radiation treatment.
                                                                                                                                                                                                                                Claim 12; Page 41-42;
                                                                                                                                                                                                                                                                Isolated mucin-1-specific binding member for diagnosing and/or treating cancer, e.g. breast cancer, comprises antigen binding domain having region that contains specific amino acid sequence –
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N-PSDB; ABX79100.
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HENDERIKX M P G.
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       N-PSDB; AAQ54655
                        WPI; 1994-007204/01
                                                                                                                 (CITY ) CITY (YANG/) YANG
                                                                                                                                                                        15-JUN-1992;
                                                                                                                                                                                                           15-JUN-1993;
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93.2%;
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                                                                                                                                                                                                                                                                       antigen; CCA; murine; mouse;
cell; light chain; tumour.
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Pred. No. 3.7e-133;
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415

DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 449

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Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents the heavy chain variable region of a rat immunoglobulin G (IgG) antibody which is specific for the CD3 antigen complex, and the human CH1-hinge-aglycosylCH2CH3. The specification describes chimeric human/rodent anti-CD3 antibodies, which have a rodent CD3 light chain variable region and a human heavy chain variable region. The anti-CD3 antibodies can render T-cells non-functional by antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex. They can be used for immunosuppression, particularly for the control of graft rejection. The antibodies can also enhance or re-direct T-cell responses to antigens. They can be used in the treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New humanized anti-CD3 antibodies, used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waldmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BTGI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200005268-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunosuppression and preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen-T-cell receptor complex; graft rejection; cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ή,
                                                                                                                                                                                                                                                                                          VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                 VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199
                                                                                                                                                                                                                                                                                                                                                                                                                     ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGEDYWGQGTR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLLESGGGLVQPGGSLRLSCAASGFTESNYAMSWVRQAPGKGLEWVSAISASGHSTYL
                                                       PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                   EEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                            ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                        ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR
                                                                                                                                                                                                                                                                      VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                             VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                   PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                               EEQYASTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Page 45-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INT LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2279; D)
Pred. No. 1.5e
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            graft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
..5e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
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QGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKI)YFPEPVTVSWNSGALTSGVH

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RESULT 8
AAE12715
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                                                                                                                                                                                                                              The invention relates to an isolated tumour-assoc.ated antigen mucin-1 (MMC-1)-specific binding member comprising an antigen binding domain (CC region having an antibody variable light (VL) or leavy (VH) region, CC or a complementarity determining region (CDR) of 'L or VH. MUCI-specific binding member is useful for diagnosing cancer, p:eferably adenocarcinoma CC binding member is useful for diagnosing cancer, p:eferably adenocarcinoma CC magnetic resonance imaging, scintillation counting, and x-ray film. CC magnetic resonance imaging, scintillation counting, and x-ray film. CC magnetic resonance imaging, scintillation counting, and x-ray film. CC magnetic binding member is useful for treating cancer, preferably CC adenocarcinoma, in an individual, where the cancer is present in tissue CC of the breast, ovary, lung, or bladder of the individual. MUCI-specific binding member is useful for diagnosing and imaging MUCI-specific CC binding member is useful for diagnosing and imaging MUCI-specific CC containing molecules, and for therapeutically or prophylactically cancer. The present sequence is human recombinant immunoglobulin CC (Ig) heavy chain region (variable VH and CH constant heavy chain).
                                                                                                                                     Matches
                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; tumour-associated antigen mucin-1; MUC-1; alenocarcinoma; heavy chain region; cancer; breast; ovary; lung; bladder; cytostatic; therapy; immunoglobulin; Ig.
                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 106-108; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated tumor-associated antigen mucin-1-specific binding member for diagnosing and treating cancer, comprises mucin-1 binding domain or its portion for binding to an epitope of the protein core of mucin-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200175110-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hoogenboom HRJM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAR-2001; 2001WO-US10589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
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)B; AAD20745.
   61
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                                                                                                                                                     Similarity
EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQLPGKGLEWVSAISASGHSTYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; Protein; 451
                                                                   QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQI,PGKGLEWVSGISGSGGSTYY
                                                                                                                                                                                                      451 AA;
                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0538913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin
                                                                                                                                                     89.8%;
93.2%;
                                                                                                                                                  Score 2257; DB 22;
Pred. No. 3.7e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                     Mismatches
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                                                                                                                                                                 Length 451;
                                                                                                                                     Indels
                                                                                                                                    12;
                                                                                                                                    Gaps
                                                                  60
                                 135
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                                            24-FEB-2000; 2000US-0184601
08-DEC-2000; 2000US-0254465
08-DEC-2000; 2000US-0254498
Holtzman
                                                                                                                                                                 Protein
                                                                                                                                                                                                              Synthetic.
                                                                                                                                                                                                                               Mus sp.
                                                                                                                                                                                                                                                 gene therapy.
                                                                                                                                                                                                                                                          Alzheimer's disease;
                                                                                                                                                                                                                                                                                   Humanised monoclonal antibody Hu266, heavy chain.
                                                                                                                                                                                                                                                                                                       04-DEC-2001
                                                                                                                                                                                                                                                                                                                                           AAU07745
                 (UNIW ) UNIV WASHINGTON (ELIL ) LILLY & CO ELI.
                                                                                26-FEB-2001; 2001WO-US06191
                                                                                                                    WO200162801-A2.
                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                   Monoclonal antibody;
                                                                                                                                                                                                                                                                                                                                                                                                         416
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Ž,
                                                                                                                                                                                                                                                                                                                                                                                     NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                       PAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTMIVVLNGG-----FDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----YYDSGGYFTVAFDIWGQGTMVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GKGLEWVSGISWDSSSIGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDMALYYCVKGRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \tt MELGLSWIFLLAILKGVQCEVQLVESGGGLVQPGRSLRLSCAASGETFNDYAMHWVRQAP
                                                                                                                                                                                                                                                                                                       (first entry)
Demattos R,
                                                                                                                                     /label= Mature_Hu266_heavy_chain
/note= "This sequence is specifically claimed
claim 17"
                                                                                                                                                                                  Location/Qualifiers
1..19
                                                                                                                                                               /label= Signal_peptide
20..461
                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                         Hu266; nootropic; neuroprotective; Abeta peptide;
Down's syndrome; cerebral amyloid angiopathy;
Bales
                                                                                                                                                                                                                                                                                                                                           461
KR,
Paul
, MS
Tsurushita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   295
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RESULT 7
AAY68810
ID AAY6
XX
AC AAY6
AC AAY6
XX
DT 16-W
XX
DE A 18
XX
KW CD3

AAY68810 standard;

Protein;

449

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AAY68810; 16-MAY-2000

(first

entry)

A rat heavy

chain region and

a human hinge region

CD3 antigen complex; chimeric antibody; immunosuppression; heavy

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TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             an epitope contained within positions 13-28 of amyloid beta peptide, Abeta. The antibody is useful to inhibit and reduce the formation of amyloid plaques or the effects of toxic soluble Abeta species in humans their fragments are used for the manufacture of a medicant. This includes the prolonged expression of recombinant sequences of them in human tissues for the treatment of clinical/pre-clinical Alzheimer's disease, Down's syndrome or pre-clinical cerebral amyloid angiopathy. Specifically, the antibody is used to sequester Abeta into plasma, brain or cerebrospinal fluid to prevent/reverse accumulation of the Abeta peptide within the brain thereby improving cognition. The present sequence is the heavy chain of a humanised monoclonal antibody, Hu266, based on the mouse antibody 266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 13; Fig 5; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vasquez M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humanised antibody for the treatment of Alzheimer's comprises ibition and reduction of the formation of amyloid plaques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention relates a humanised antibody that specifically binds
                                                                                                                                                                                                             168
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              421
                                         348
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                                                                                                                                                                                                                                                                                                                                                                                                                                    435;
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                                                                                                                                                                                                                                                                                                                                                                                          1 MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                        VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                        KTISKAKGOPREPOVYTLPPSREEMTKNOVSLTCLVKGFYPSDIAVEWESNGOPENNYKT
                                                                                              GKGLELVAQINSVGNSTYYPDTVKGRFTISRDNAKNTLYLQMNSLRAEDTAVYYCASG--
                                                                                                                                                                                                                                                                                                                                    GKGLEWVSAISASGHSTYLADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE 120
                                                                                                                                                                                                                                                                                                                                                                              MNFGLSLIFLVLVLKGVLCEVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMSWVRQAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         461
                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                              91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 2304.5; DB 2
Pred. No. 4.1e-136;
3; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22;
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  망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chumanised antibody of the present invention. In the variable cregion of this sequence, the complementarity determining regions (CDRs) originate from murine monoclonal antibody 3D6 and the framework region from human germline VH segment DP-45 and J segment that Novel humanised antibodies of the invention have CDRs from 3D6 and human framework sequences. These humanised antibodies have binding affinities (affinity and epitope location) approximately the same as those of the mouse 3D6 antibody. The invention includes antibodies, single chain antibodies, and their fragments, as well as nucleotide sequences, vectors, transformed host cells, and methods of using the humanised antibody to treat, prevent, alleviate, reverse or otherwise ameliorate symptoms and/or pathology associated with Down's syndrome, (pre-)clinical anyloid angiopathy, and to inhibit formation or reduce Abeta plaque in the brain.
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Best Local S
Matches 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13-14; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tsurushita N,
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                                                                                                 KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                 VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
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KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
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91.6%;
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Pred. No. 9.1e-137;
6; Mismatches 18;
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Matches

438;

Conservative

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Mismatches

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Gaps

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RESULT 5
AAR20057
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Query Match
Best Local Similarity
                                            The variable region of the heavy chain is upprotein with the variable region from the kethe two V regions being joined by a linker. binds to HIV gp160.
                                                                                              Recombinant protein which binds to complex viral antigen a HIV-1 - contains variable region of antibody derived from cell line, used for detecting HIV-1 antigen
                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                           Region
                      Sequence
                                                                                 Claim 2;
                                                                                                                                                  Felgenhauer M,
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DB; AAQ20066.
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                                     AAQ20067 and
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146..47
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91.98;
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Score 2309.5; DE Pred. No. 2e-136;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                      The invention relates to polynucleotides encoding novel human controlled in a method of contibodies raised against the polypeptides are used in a method of treatment of a mammal and prevention of disorders caused by the aberrant controlled respectively. The polypeptides can be used as controlled respectively. The polypeptides can be used as protein expression or activity. The polypeptides can be used as controlled respectively and in antibody production. The polypeptides are used to identify compounds which bind to the controlled respectively. The polypeptides and proteins and in generating anti-sense DNA or controlled respectively. The invention are used as probes and controlled respectively. The polypeptides and in generating anti-sense DNA or controlled respectively. The invention can be used to controlled respectively. The invention can be used to controlled respectively. The invention can be used to controlled respectively. The invention is tissue markers, and to isolate receptors or ligands. Controlled respectively are called the controlled respectively. The invention can be used to controlled respectively. The invention is the controlled respectively. The invention is the controlled respectively. The invention can be used to controlled respectively.
                                                                                                         fungal infection or from autoimmunity, cancer, allergy, asthma,
graft-versus-host disease, eczema, haemophilia, thrombosis,
anti-inflammatory diseases, nervous system disorders, and infec-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tang
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thrombolytic; immunogen; antibody; gene therapy; neu
Parkinson's disease; inflammatory disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; novel protein; Antianaemic; osteopathic; antiinflammatory; immunomodulatory; cytostatic; neuroprotective; vulnerary; nootropic; anticonvulsant; antiarthritic; cerebroprotective; antifungal; antiarthritic; antibacterial; antialtergic; dermatological; haemostatic; antiasthmatic; thrombolytic; immunogen; antibody; gene therapy; neurological disorder; ParkInson's disease; inflammatory disorder; cancer; asthma; osteoporosis.
       Sequence
                                                                                                                                                                                                       the proliferation, differentiation and survival of stem cells, as a contraceptive, treating osteoporosis and osteoarthritis, anaemia, Alzheimer's, Parkinson's and Huntington's diseases, amylotrophic lateral sclerosis, stroke, immune deficiencies resulting from bacterial, viral o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated polypeptides useful for treating anti-inflammatory diseases, nervous system disorders, and for regenerating bone and cartilage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAS22593
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118..12
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20..468
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RESULT 2
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AC ABU0
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AC ABU0
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DF 10-M
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KW Huma
KW MAb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents the heavy chain protein of the monoclonal antibody from clone JA. The invention relates to an isolated human monoclonal rabies virus neutralising antibody (virucide) derived from cDNA clones encoding the antibody heavy and light chains expressed in heterologous expression systems and purified away from deleterious contaminants. The invention provides a fused gene encoding a chimeric immunoglobulin light chain and a fused gene encoding a chimeric immunoglobulin heavy chain. The antibody of the invention is useful for treating an individual exposed to a rabies virus by administering to the individual a therapeutically effective amount of the antibody, and preventing a spread of the rabies virus to the central nervous system (CNS). The antibody of the invention provides a safe and efficacious positions.
            Human; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rables; neurological disease; infection; central nervous system; rables virus; lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; heavy chain.
                                                                                             10-MAY-2003
                                                                                                                    ABU08017
                                                                                                                                          ABU08017 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exposure prophylactic therapy for individuals exposed to a rabies virus
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                                                                                                                                                                                                                                                                                                                                                                                      TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                             KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT
                                                                                                                                                                                                                                                                                                                                                                                                             VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK
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                                           RVEPKSCDKTHTC.PPCPAPELLGGPSVFLFPPKPKDTLMI:RTPEVTCVVVDVSHEDPEV
                                                                                                                                                    VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSL(:TQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                 VTMIVVLNGGEDYWGQGTRVTVSSASTKGPSVFPLAPSSK%TSGGTAALGCLVKDYFPEP
                                                                                                                                                                                                                                              GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYL(MNSLRAEDTAVYYCAKDRE
                                                                                                                                                                                                                                                                                           MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSC AASGFTFSNY AMSWVRQAP
                                                                                                                                        GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYL(:MNSLRAEDTAVYYCAKDRE
                                                                                                                                                                                                                                                                                MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLS( AASGFTFSNYAMSWVRQAP
                                                                                                                                                                                     VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSK!/TSGGTAALGCLVKDYFPEP
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Conservative

0;

0,

Indels Length

0;

Gaps

240

180

240

420 420 360 360 300 300 180

120

60

120

Score 2514; DB 24; Pred. No. 3.4e-149; Mismatches

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The invention discloses a recombinant antibody comprising a constant cregion of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable cregion. Rables is an acute, neurological disease caused by infection of the central nervous system with the rables virus, a member of the CL Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods cromportion of the family Rhabdoviridae. Also disclosed are methods cromportion of the family Rhabdoviridae. Also disclosed are methods cromportion of the combinant antibody by sulturing a host cell, containing a recombinant expression vector comprising the nucleic acid conclecule encoding the antibody, and isolating the recombinant antibody capressed and treating an individual exposed to a pathogen by compressed and treating an individual exposed to a pathogen, e.g. rables infection. They are also useful for the gualitative and guantitative determination of the rables virus. The sequences presented are the antibody protein fragments, the nucleic acids concoding them or the PCR primers used to construct the recombinant conversion vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New recombinant antibody comprising a constant region to a non-Mab 57 variable region, useful for treating a exposed to a pathogen, e.g. rabies infection
                                                                                                                                                                                                       expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Page 32-33; 38pp; English.
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Perfect score:
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Gapop 10.0 , Gapext 0.5
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2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981 DAT: *
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1982 DAT: *
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Heavy chain of 3D6
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                                        Humanised monoclon
A rat heavy chain
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ALIGNMENTS

RESULT 1
ANAOLY 1
ANAOLY 2
ANA HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain; human monoclonal rabies virus neutralising antibody; immunoglobulin; light chain; central nervous system; CNS; prophylactic therapy; clone JA. Hooper DC, (UYJE-) UNIV JEFFERSON THOMAS 16-MAY-2000; 2000US-204518P. 04-MAY-2001; 2001WO-US14468 22-NOV-2001 WO200188132-A2 Homo sapiens. Heavy chain protein of the monoclonal antibody from clone 07-MAY-2002 AAO14065; AAO14065 standard; Protein; 474 Dietzschold (first entry) , B; ₽ JA

WPI; 2002-062381/08. N-PSDB; AAK98701.

Novel isolated human monoclonal rabies virus neutralising antibody

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Result
No.
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       100.0
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88.8
88.0
87.2
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86.4
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Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-848-332-4
US-10-153-382-1
US-10-153-382-15
US-10-153-382-11
US-09-859-053-38
US-09-859-053-38
US-09-453-234-82
US-09-453-234-98
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US-10-225-108A-4
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US-10-171-452A-56	US-10-171-452A-38	US-09-453-234-72	US-09-453-234-40	US-09-453-234-78	-453	US-10-150-475A-4	US-10-006-593-69	US-09-453-234-42	w	US-09-453-234-38	-026-925-	US-10-159-006-36	-453-	US-09-453-234-50	9	US-09-972-656-100	-10	US-09-453-234-86	. US-10-006-593-118	US-09-453-234-74	US-09-791-153A-47	0-216-	US-10-216-484-52	US-09-740-002-24	US-10-216-484-131	-10-216-484-	US-10-216-484-109	-10-221-945-	US-10-216-484-50
56,	Sequence 38, Appl	72,	40,	Sequence 78, Appl	44,	4		42,	52,	Sequence 38, Appl	55,	36,		50,	22,	100	54,	Seguence 86, Appl	118		47,	127,	e 52,	24, Ap	131,		109,	1, A	Sequence 50, Appl

ALIGNMENTS

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                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HOOPER, Craig
APPLICANT: HOOPER, Craig
TITLE OR INVENTION: Recombinant Antibodies, and Compositions
TITLE OF INVENTION: and Methods for Making Them
FILE REFERENCE: 8321-110
CURRENT APPLICATION NUMBER: US/10/225,108A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 09/848,832
PRIOR APPLICATION NUMBER: US 60/204,518
PRIOR FILING DATE: 2001-05-04
PRIOR FILING DATE: 2001-05-16
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/314,023
PRIOR FILING DATE: 2001-08-21
NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 4
                                                                                                                                                                                                                                           LENGTH: 234
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                        Local Similarity
                                                                                                                                                  234; Conservative
 61
                 61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLE; PEDFAVYYCQQRFNWPWTFGQ 120
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                                                                                                                                              Score 1223; DB 14.
Pred. No. 1.2e-72;
Pred. No. 1.2e-72;
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; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo s
US-10-153-382-7
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US-10-153-382-7
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                                                                                                                                                                           Sequence 7, Application US/10153382
Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
DUTTO NOTE: 2002-05-22
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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   Query
                                                                                                     SEQ ID NO 7
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                                                                                                                              CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
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APPLICANT: Dietzschold, Bernhard
APPLICANT: Dietzschold, Bernhard
TITLE OF INVENTION: RABIES VIRUS-SPECFIC NEUTRALIZING HUMAN
TITLE OF INVENTION: MONOCLONAL ANTIBODIES AND NUCLEIC ACIDS AND RELATED METHODS
FILE REFERENCE: HOOO1.NP0002
                                                                                                                    SOFTWARE: PatentIn
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Pred. No. 1.2e-72;
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US-10-153-382-15
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Publication No. US20030086930A1
GENERAL INFORMATION:
APPLICANT: PFIZER PRODUCTS INC.
                                                                                                               GENERAL INFORMATION:
                                                                                                                              Sequence 11, Application US/10153382 Publication No. US20030086930A1
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SEQ ID NO 15
LENGTH: 234
TYPE: PRT
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Best Local :
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                                                               APPLICANT: PFIZER PRODUCTS INC.
TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
FILE REFERENCE: PC23019A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES FILE REFERENCE: PC23019A
CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/233042
PRIOR APPLICATION NUMBER: 60/233042
PRIOR FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 39
                              CURRENT APPLICATION NUMBER: US/10/153,382
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: 60/293042 PRIOR FILING DATE: 2001-05-23
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les 213; Conservative
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Pred. No. 2.3e-64;
6; Mismatches 15
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SEQ ID NO 34
LENGTH: 236
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SEQ ID NO 11
LENGTH: 233
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Best Local Similarity
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APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/9/859,053
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: JP 2001-9508
PRIOR FILING DATE: 2001-05-18
PRIOR FILING DATE: 2001-05-18
NUMBER OF SEQ ID NOS: 43
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Best Local :
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TYPE: PRT
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Pred. No. 4.6e-63;
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US-09-453-234-82
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US-09-859-053-38
                                                                                                                                                      APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
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                                     SEQ ID NO 82
LENGTH: 224
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Publication No.
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APPLICANT: Tezuka, Katsunari
APPLICANT: Tezuka, Katsunari
APPLICANT: Hori, No. US20020102658Aluaki
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
FILE REFERENCE: 06501-079001
CURRENT APPLICATION NUMBER: US/09/859,053
CURRENT FILING DATE: 2001-05-16
CURRENT FILING DATE: 2001-05-16
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PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 43
                                                                          PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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ORGANISM: Homo sapiens
                    TYPE: PRT
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89.4%;
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Pred. No. 2e-62;
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; SEQ ID NO 88
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-34L
US-09-453-234-88
RESULT 10
US-09-453-234-90
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US-09-453-234-88
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APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
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                                                         LSKADYEKHKYYACEVTHQGLSSPVTKSFNRGE 233
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                                                                                                     SDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLT 200
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95.8%;
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Pred. No. 7.5e-62;
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; OTHER INFORMATION: M2-35L
US-09-453-234-90
                                                                       US-09-453-234-36
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US-09-453-234-36
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 90
LENGTH: 224
TYPE: PRT
                                                                                                                                        SOFTWARE: PatentIn Ver. SEQ ID NO 36
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                  Query Match
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Best Local
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Best Local Similarity Matches 204; Conserv
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                                                                                                                                                                                                                          APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
                                                                                       LENGTH: 224
TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
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Lonbor
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Biosite Diagnostics,
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                  86.2%;
95.8%;
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Pred. No. 7.5e-62;
3; Mismatches 6;
Score 1054; DB 11;
Pred. No. 1.2e-61;
2; Mismatches 7;
                                  Length 224;
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APPLICANT: Walkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
APPLICANT: Gray, Jeff
APPLICANT: Lonberg, Nils
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Belosite Diagnostics, Inc.
APPLICANT: GenPharm International
ITITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-0001100S
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 84
LENGTH: 224
TYPE: PRT
                                               US-09-453-234-46
; Sequence 46, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
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Best Local
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   APPLICANT: Buechler, Joe
APPLICANT: Valkirs, Gunars
APPLICANT: Gray, Jeff
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-453-234-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
OTHER INFORMATION: M2-32L
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                                                                                                                                                               LSKADYEKHKYYACEVTHQGLSSPVTKSFNRGE 233
                                                                                                                                                                                                                             RFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSVFIFPP 140
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Pred. No. 4.5e-61;
3; Mismatches 8;
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APPLICANT: GenPharm International
ITTLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PATENTIN UNS: 112
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 46
                                                                                                                                                                                                                          APPLICANT: Tamaki, İkuko
APPLICANT: Takahashi, Tohru
TITLE OF INVENTION: Anti-Fas Antibodies
FILE REFERENCE: 9801.26CIP/HG
CURRENT APPLICATION NUMBER: US/10/216,484
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/99/499,662
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 2000-02-09
PRIOR FILING DATE: 1998-04-01
NUMBER OF SEQ ID NOS: 165
SEQ ID NO 107
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; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORWATION: M1-10L
US-09-453-234-46
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                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: Designed light ; OTHER INFORMATION: chain of humanized anti-Fas ant.:body US-10-216-484-107
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US-10-216-484-107
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APPLICANT: Haruyama, Hideyuki
APPLICANT: Nakahara, Kaori
                                                                                                                                                                                              LENGTH: 23
TYPE: PRT
                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                 FEATURE:
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MEAPAQLLFLLLUMLPDTTGEIVLTQSPATLSLSPGERAT).ACRASQT----ASRYLAWY
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Biosite Diagnostics, Inc.
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                                                84.0%; Score 1027; DB 15; ilarity 84.5%; Pred. No. 7.1e-60; Conservative 11; Mismatches 22;
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Pred. No. 6 1e-61;
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GENERAL INFORMATION:

APPLICANT: TSuji, Takashi

APPLICANT: TSuji, Takashi

APPLICANT: TSuji, Takashi

APPLICANT: HOTI, NO. US20020102658Aluaki

PTITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

TITLE OF INVENTION: COSTINULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

TITLE OF INVENTION: HARMACEUTICAL USE THEREOF

FILE REFERENCE: 06501-079001

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT APPLICATION NUMBER: US/09/859,053

CURRENT APPLICATION NUMBER: JP 2001-99508

PRIOR APPLICATION NUMBER: JP 2001-99508

PRIOR APPLICATION NUMBER: JP 2000-147116

PRIOR APPLICATION NUMBER: JP 3000-147116

PRIOR APPLICATION NUMBER: JP 3000-147116

SOFTWARE: FRSKESEQ for Windows Version 4.0

SEQ ID NO 30

LENGTH: 236
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US-09-859-053-30
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Search completed: September 12, Job time: 16.2034 secs
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                                                              GNSQESVTEODSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 238
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Perfect score:
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     Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/pcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-276-852-153
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US-08-899-575-153
US-08-812-586-16
US-08-812-586-16
US-09-335-832A-17
US-07-916-098A-6
US-08-480-753-6
US-09-041-889-11
US-09-041-889-11
US-09-417-264-11
US-09-417-264-11
US-09-417-264-79
US-08-487-058-6
US-08-487-550-6
US-08-487-550-6
US-09-171-945-97
US-08-485-737B-69
US-09-485-16-12
US-09-485-16-12
US-09-48-744-80
US-09-740-002-26
US-09-740-002-26
US-09-301-593-28
US-07-9301-593-28
US-07-934-373-25
US-08-437-642B-25
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US-09-049-672A-6
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76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.6	76.7	76.7	76.7	76.9	77.0	77.0
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US-09-460-587-6	US-09-607-756-2	US-09-422-712B-2	US-09-097-171A-10	US-09-097-309-6	PCT-US93-07832-40	US-09-460-587-2	US-09-097-171A-2	US-09-097-309-2	US-08-437-642B-40	US-08-788-800-11	US-07-934-373C-40	PCT-US93-07832-39	US-08-437-642B-39	US-07-934-373C-39	US-08-480-753-8	PCT-US93-07832-25	US-08-146-206C-25
Sequence 6, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 10, Appl	Sequence 6, Appli	Sequence 40, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 40, Appl	Sequence 11, Appl	Sequence 40, Appl	Sequence 39, Appl	Sequence 39, Appl	Sequence 39, Appl	Sequence 8, Appli	Sequence 25, Appl	Sequence 25, Appl

ALIGNMENTS

Sequence 6, Approximately No. 613594 Patent No. GENERAL II COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR WI
CURRENT APPLICATION NUMBER: US/O
FILING DATE: HEREWITH
CLASSIFICATION UMBER: 536
PRIOR APPLICATION UMBER:
APPLICATION NUMBER:
FILING DATE:
FILING DAT INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: STRANDEDNESS: S
TOPOLOGY: linea
IMMEDIATE SOURCE: APPLICANT: APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28 TELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555 ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,7
REFERENCE/DOCKET NUMBER: CORRESPONDENCE ADDRESS: APPLICANT: STREET: 3174 PO: CITY: Palo Alto STATE: CA TELEX: ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive LIBRARY: LENGTH: INFORMATION: amino acid Application US/09049672A Tang, Y. To Yue, Henry 234 amino acids 650-845-4166 Lal, Preeti Hillman, Jennifer L. FastSEQ for Windows Version linear IBM Compatible single US/09/049,672A 39,132 6. PF-0497 US 2.0

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RESULT 3
US-09-301-593-36
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US-09-049-672A-6
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Best Local S
Matches 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: NEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT APPLICATION NUMBER: 09/335,697
PRIOR FILLING DATE: 1999-06-18
PRIOR FILLING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILLING DATE: 1995-06-07
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SOFTWARE: PatentIn Ver. 2.1
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01; Conservative
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                                                                                                             ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                                                                               GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
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80.8%; Pred. No. 1e-7
tive 16; Mismatches
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LENGTH: 240
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                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: BUTCON, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 170
CORRESPONDENCE ADDRESS:
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APPLICANT: Garin-Chesa,
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ORGANISM: Homo sapiens
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                  SOFTWARE: PatentIn Release #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                          ADDRESSEE: The Scripps Research Institute, Office ADDRESSEE: Patent Counsel STREET: 10666 No. 5652138th Torrey Pines Road, Sui STREET: Mail Drop TPC8 CITY: La Jolla STATE: CA
                                                                                                                                              COUNTRY: USA
ZIP: 92037
   FILING DATE:
                     APPLICATION NUMBER:
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Pred. No. 8.
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Length 240; Indels

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US-08-899-575-153
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Best Local Similarity 82.1
Matches 193; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
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APPLICATION NUMBER: US 07/954,148

FILLING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 619-554-6312 INFORMATION FOR SEQ ID NO: 153:
                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,575
FILING DATE: 24-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                           APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                       ADJAKESSEE: Patent Counsel
STREET: 10666 No. 5770440th Torrey Pines Road, Suite 220,
STREET: Mail Drop TPC8
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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CLASSIFICATION:
                                                                                                                                             COUNTRY: UZIP: 92037
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82.1%; Pred. No. 1.6e-72;
tive 14; Mismatches 27;
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; MOLECULE TYPE: protein US-08-899-575-153
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US-08-899-575-153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5804440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sig
Matches 193;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Burton, Dennis R
APPLICANT: Barbas, Carlos F
APPLICANT: Lerner, Richard A
TITLE OF INVENTION: HUMAN NEE
TITLE OF INVENTION: TO HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 619-554-2937
                                                                                                                                                                 COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 30-SEP-1992 ATTORNEY/AGENT INFORMATION:
                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                           ADDRESSEE: Patent Counsel STREET: 10666 No. 5804440th Torrey Pines Road, Suite 220. STREET: Mail Drop TPC8
                                   APPLICATION NUMBER: US/08/899,575 FILING DATE: 24-JUL-1997
                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                          SOFTWARE:
                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                  ADDRESSEE: The Scripps Research Institute, Office of ADDRESSEE: Patent Counsel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 30-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/276,852 FILING DATE: 18-JUL-1994
                   CLASSIFICATION
                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 QESVTEQDSKDSTYSLSSTLTLSKADYEKHKYYACEVTI QGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 QESVTEQDSKDSTYSLSSTLTLSKADYEKHKYYACEVTLQGLSSPVTKSFNRGEC 235
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CA
USA
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                                                                                                                                                                                                                                           Jolla
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                                                                                        PatentIn Release #1.0, Version
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                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                             HUMAN NEUTRALIZING MONOCLONAL ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80.0%; Score 978.5; DB 1;
82.1%; Pred. No. 1.6e-72;
Live 14; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                           170
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RESULT 7
PCT-US95-08743-153
Sequence 153, Application PC/TUS9508743
GENERAL INFORMATION:
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   Best Loc
Matches
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                                  Query Match
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Best Local Similarity
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APPLICATION NUMBER: US 07/954,148

FILING DATE: 30-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: FILTING, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: SCR1452P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 619-554-6312
INFORMATION FOR SEQ ID NO: 153:
SEQUENCE CHARACTERISTICS:
                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/08743
FILING DATE: 11-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/276,852
FILING DATE: 18-JUL-1994
                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 619-554-2937
TELEFAX: 619-554-6312
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                                                                                                         LENGTH: 235 amino acids
TYPE: amino acid
   Local Similarity
nes 193; Conserv
                                                                                               TOPOLOGY:
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   Conservative
                                                                                               linear
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                                                                               protein
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18-JUL-1994
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                80.0%; Score 978.5;
82.1%; Pred. No. 1.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 978.5; DB 1; 82.1%; Pred. No. 1.6e-72; tive 14; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/178,302
 Mismatches
                 1.6e-72;
                              DB 5;
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 27;
                              Length
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US-08-812-586-16
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                                                                                                                                                                  Query Match
                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                            TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Martin Da
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1185 Ave.
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                               Local
                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/812,586 FILING DATE: 07-MAR-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120 QGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS 179
                                61 GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
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                                                                                                                                              h 80.0%;
Similarity 84.1%;
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MRVPAQLLGLLLLWLPGARCAIRIAQSPSSLSASTGDRVTITCRASQGISNYLAWYQQKP
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1185 Avenue of the Americas
                                                                                                                                  Conservative
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MENTION: PURIFIED AND RECOMBINANT ANTIGENIC
MENTION: PURIFIED AND RECOMBINANT ANDOMINAL AORTIC ANEURYM (AAA)
JENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
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                                                                                                                                               Score 978; DB 3; Pred. No. 1.7e-72;
                                                                                                                                  Mismatches
                                                                                                                                                               DB 3; Length 235;
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                                                                                                                                    29;
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US-09-535-832A-17
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APPLICANT: Tilson, Martin David
APPLICANT: Tilson, Martin David
TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
TITLE OF INVENTION: With Abdominal Aortic Aneurysm (AAA) Disease, and
TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 17, Application US/09535832A
Patent No. 6537769
                                                                                                                                                                                                                                                                                                                                              Sequence 56, Application US/07916098A Patent No. 5871732
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                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: BURKLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 53862-AZ
CURRENT APPLICATION NUMBER: US/09/535,832A
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NUMBER OF SEQ ID NOS: 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 235
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD
STREET: 10 SOUTH WACKER DRIVE
                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                     CITY: CHICAGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
   OPERATING SYSTEM:
                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQAPRLLIYDASSRATGIPDRFSGSGSGTDFTLTISRLEPEDFAVYYGQQYGSSPLTFGG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 235
                                                                                                    ILLINOIS
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                                                                                                                                                                                                                                        ROSA, MARGARET D. ROSA, JOSEPH J.
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                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                             BURKLY, LINDA C
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   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.0%;
                                                                                                                                                                                                        ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN PROPHYLAXIS AND TREATMENT OF AIDS, AI
                                                                                                                                                                                                                                                                                            PATRICIA L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
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US-08-480-753-6
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS FOR SELECTIVELY DETECTING
TITLE OF INVENTION: PERINUCLEAR ANTI-NEUTROPHIL CYTOPLASMIC ANTIBODY
TITLE OF INVENTION: ULCERATIVE COLITIS, PRIMARY SCLEROSING CHOLANGITI
TITLE OF INVENTION: TYPE I AUTOIMMUNE HEPATITIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
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NAME: JOHN J. MC DONNELL
                                                                                                                                                                                                                                                                                        APPLICANT: Targan M.D., Stephan R. APPLICANT: Vidrich Ph.D., Alda M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                 COMPUTER:
OPERATING
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TELEX: 910/221-5317
TELEX: 910/221-5317
                                                                                                                  STREET: 444 South
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/
FILING DATE: July 24, 1992
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                                                                                                       COUNTRY:
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REFERENCE/DOCKET · NUMBER: 92
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                                                                                                                                                                      ADDRESSEE:
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190; Conserv
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||||||| |:||| | | |:|:| |||||||||||:::
WYQQKPGQPPKLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQAEDVAVYYCQQYYSY 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MRVPAQLLGLLLLMLPGARGDIVMTQSPDSLAVSLGERATINCKSSGSLLYSTNQKNYLA 62
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                                                                                                                                                    E: Wendy A. Whiteford, E. 444 South Flower Street,
IBM PC compatible SYSTEM: PC-DOS/MS-DOS PatentIn Release #1.0,
                                                                                                     USA
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(312) 715-1234
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NN: 424
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5871732ember 27,
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Whiteford, Esq.
freet, Suite 2000
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; Pred. No. 7.3e-72;
18; Mismatches 25;
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 Version #1,25
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

07-JUN-1995

US/08/480,753

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-041-889-11
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 11, Applicativation Patent No. 6033864
GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acids
                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof,
TITLE OF INVENTION: Microbial UC pANCA antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 36,964
REFERENCE/DOCKET NUMBER: POTELECOMMUNICATION INFORMATION:
                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                             APPLICATION NUMBER: US 01
FILING DATE: 11-APR-1997
ATTORNEY/AGENT INFORMATION:
                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       CITY: San Diego
STATE: California
   REGISTRATION NUMBER:
                                                                                              CLASSIFICATION:
                                                                                                              FILING DATE:
                                                                                                                             APPLICATION NUMBER:
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                 Campbell,
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                                                                                                                                                                                                                                                                                                  EE: Campbell & Flores LLP 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09041889
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Cathryn A.
BER: 31,815
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88.7%;
                                                             US 08/837,058
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Pred. No. 2.8
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US-08-837-058-11
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Patent No. 6
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                                                                                                            APPLICATION NUMBER: US/08/837,0 FILING DATE: CLASSIFICATION: 435 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815 REFERENCE/DOCKET NUMBER: P-PM 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                    TELEFAX: (619) 535-89
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Braun, Jonatha
APPLICANT: Targan, Stepha
APPLICANT: Eggena, Mark
TITLE OF INVENTION: Diagn
TITLE OF INVENTION: Ulcer
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC. COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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SEQUENCE CHARACTERISTICS:
LENGTH: 214 amino acid
                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Diagnosis, Prevention and Treatment of TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtypes Thereof, TITLE OF INVENTION: Histone H1
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LENGTH: 214 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                              STATE:
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Local Similarity 88.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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Pred. No. 2.
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                                                       ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-09-417-264-11
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US-09-417-264-11
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             Query Match
Best Local Similarity
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                                                                                                                                           TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Braun, Jonathan
APPLICANT: Cohavy, Offer
TITLE OF INVENTION: Diagnosis, Prevention and Treatment of
TITLE OF INVENTION: Ulcerative Colitis, and Clinical Subtyr
TITLE OF INVENTION: Microbial UC pANCA antigens
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-PM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: I
                                                                                                                            SEQUENCE CHARACTERISTICS:
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CITY: San Diego
STATE: California
COUNTRY: USA
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                                                                                                   TYPE: amino acid
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4370 La Jolla Village Drive, Suite 700
                                                                                                            214 amino acids
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Pred. No. 2.8e-71;
              Score 962.5; DB Pred. No. 2.8e-71
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GENERAL INFORMATION:

APPLICANT: ES van, Helmuth
APPLICANT: Havenga, Menzo
APPLICANT: Verlinden, Stefan
TITLE OF INVENTION: TARGETED DELIVERY THROUGH A (
FILE REFERENCE: 2183-4080US
CURRENT APPLICATION NUMBER: US/09/315,926A
CURRENT FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 99201593.3
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: EP 98201693.3
PRIOR FILING DATE: 1999-05-20
PRIOR FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Patentin version 3.0
SEQ ID NO 79
LENGTH: 236
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; COTION: (1)..(236)
; OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-79
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US-09-315-926A-79
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                                                                                                                                                                                                                                Matches 194;
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                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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Similarity 82.9%;
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ESYTEQDSKDSTYSLSSTLTLSKADYEKHKYYACEVTHQ@LSSPVTKSFNRGEC
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Pred. No. 3.
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Q91W59
Q91W59
Q91W59
Q91A5
Q8TBC9
Q8N355
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                                                                                                                                                Q8NEK0
                                                                                                                                                         Q8NEK1
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                                                                                                                                                                                                              SUMMARIES
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                  Q8nck() homo
Q8tcd() homo
Q99m37 mus
Q8vcp() mus
Q8vcp() mus
Q8vc16 mus
Q8v616 mus
Q8v656 mus
Q91vf8 mus
Q91vf9 mus
Q91vf2 mus
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homo sapien
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338	343.5	352	357	357	357	358.5	362.5	368	377.5	378	379	379.5	379.5	380.5	390	392	393.5	402	404	410.5	430.5	431.5	438.5	440	440.5	443	447	453
27.6																												
127	112	114	298	111	109	106	107	108	112	235	240	114	112	107	233	108	134	116	108	236	109	109	233	237	109	237	236	108
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092589	08K1F0	Q9UL80	Q9QYF0	Q920E9	Q920E6	Q9U410	Q9UL81	Q9UL70	Q8K1F3	Q99M11	Q8WUK3	Q8K1F1	Q8K1F2	Q96SA9	Q96I69	Q9UL79	Q8VDD0	Q96PF6	Q9UL77	096E61	Q9UL86	Q9UL85	Q8N5F4	Q8WUK4	Q9UL78	Q8WTU6	Q8NEJ1	Q9UL83
mus	Bug	homo	Q9qyf0 mus musculu	Bum	Q920e6 mus musculu	schis	homo	Q9u170 homo sapien	mus		homo	Bum	mus	homo	homo	-	0 mus	homo	homo	homo	Q9ul86 homo sapien	homo	Q8n5f4 homo sapien	homo	Q9u178 homo sapien	homo	1 homo	Q9u183 homo sapien

ALIGNMENTS

Q8NEK1 PRELIMINARY; PRT; 234 AA.
Q8NEK1;
Q1-QCT-2002 (TrEMBLrel. 22, Created)
Q1-QCT-2002 (TrEMBLrel. 22, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)

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RESULT 1
ID OBNET
ID OBNET
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Best Local S
Matches 207
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A Strausberg R;

L Submitted (JUN-2002) to the EMBL/GenBank/DDBJ da:abases.

EMBL; Bc030813; AAH30813.1; -.

R InterPro; IPR007110; Ig-1ike.

R InterPro; IPR003597; Ig_cl.

R InterPro; IPR003596; Ig_WHC.

R InterPro; IPR003596; Ig_V.

R Pfam; PF00047; ig; 2.

R Pfam; PF00047; ig; 2.

R SMART; SM00407; IGC1; 1.

SMART; SM00406; IG_K; 1.

R PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebraka; Euteleostomi;
Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                ch 89.1%; Score 1090; DB 4; sl Similarity .88.5%; Pred. No. 4.6e-96; 207; Conservative 15; Mismatches 12;
61 GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                           \vdash
                                                                                  Length 234;
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RESULT Q8TCDO
ID Q8
AC Q8
AC Q8
DT 01
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Best Local S
Matches 185
                             OSTCDO PRELIMINARY;
OSTCDO;
O1-JUN-2002 (TrEMBLrel. 2
O1-JUN-2002 (TREMBLrel. 2
O1-MAR-2003 (TREMBLREL. 2
Hypothetical protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUN-2002) to the EME Submitted (JUN-2002) to the EME Submitted (JUN-2002) to the EME Submitted (JUN-2003) and submitted (June 1970) to the EME Submitted (
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01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 2.

SMART; SM00407; IGc1; 1.

SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS00290; IG_MHC; 1.
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Homo saplens (Human).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
NCBI_TaxID=9606;
      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8NEK0
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SEQUENCE 2
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      Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           al protein.
239 AA; 2
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                                                                                                                                                                                                                                 PRELIMINARY;
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77.4%;
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23,
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                                                                                            Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 961.5;
Pred. No. 9.1e
20; Mismatches
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   Craniata;
                                                                                                                                                                                                                                 PRT;
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   Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e-84;
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      Euteleostomi;
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Q99M37
ID 099W
AC Q99W
AC Q99W
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DT 01-
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                                                                                            Query Match
Best Local S
Matches 135
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Best Local S
Matches 180
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Q99M37; O1-JUN-2001 (TrEMBLrel. 17, Crea
01-JUN-2001 (TrEMBLrel. 17, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
                                                                                                                                                                                                                    Strausberg R.;
Strausberg R.;
Submitted (JAN-2001) to the EMB
EMBL; BC002035; AAH02035.1; -.
HSSP; P01679; ZFBJ.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LKKE; 2.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26344 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (FEB-2002) to the EME EMBL; BC022362; AAH22362.1; -. InterPro; IPR007110; Ig-1ike. InterPro; IPR00703006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; Ig; 2. SMART; SM00406; IGy 1. PROSITE; PS00835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKYYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STFGQGTKLEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQ
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                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78.2%;
75.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26234 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates; Catarrhini; Hominidae;
                                                                                                                             59.6%;
56.5%;
                                                                                                44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL/GenBank/DDBJ
                                                                                                                          Score 729;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 956.5; DB 4;
Pred. No. 2.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FACEDC3A3B03871D CRC64;
                                                                                                                                                                                                                             FB2B06A0B801330A CRC64;
                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238
                                                                                                                                 .5e-61;
                                                                                                                                                           DB 11;
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Best Local :
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
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01-MAR-2002 (TIEMBLrel. 20, Last sequence update)
01-MAR-2003 (TIEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
Mus musculus (Mouse).
Eukaryota: Metaon.
                                                                  Q8VCI6 PRELIMINARY; PRT; 238 AA.
Q8VCI6;
Q1-MAR-2002 (TrEMBLrel. 20, Created)
Q1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 26.2 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VCPO
Q8VCPO;
01-MAR-2002
  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 234 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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137; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                          ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25702 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 724; DB 11;
Pred. No. 4.5e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ databases
  Craniata; Vertebrata; | Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                102551C58AC2FA9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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  Euteleostomi;
; Murinae; Mus
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; Murinae; Mus
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Best Local
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Best Local
                                                                                                                                                                                                                                                                                                                                                       Submitted APR-2002) to the EMF
EMBL; BC027418; AH27418.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00396; Ig_v.
Pfam: PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
SEQUENCE 238 AA; 26224 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8R062 PRELIMINARY; PRT; 234 AA. 08R062; O1-JUN-2002 (TrEMBLrel. 21, Created) 01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-MAR-2003 (TrEMBLrel. 23, Last annotation update) Hypothetical 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                        Hypothetical SEQUENCE 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
[1]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
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     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 56.1
34; Conservative
                                                                                                                                                                              Similarity
  GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVV(:LLNNFYPREAKVQWKVDNALQ 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPG::RATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MMSSAQFLGLLLLCFQGTRCDIQMTQTTSSLSASLG`DRVTISCSASQGISNYLNWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YLQKPGQSPKLLIYKVSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCSQSTHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PTFGGGTKLEIKRADAAPTVSIFPPSSEQLTSGGASVV(:FLNNFYPKDINVKWKIDGSER
                                                                                                                                                                                                                                                        11 protein.
234 AA; 2
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
                                                                                                                                                                                                                                                           25857 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58.9%;
56.1%;
                                                                                                                                                    58.0%; Score 709; DB 1.; 58.1%; Pred. No. 1.2e-59; tive 36; Mismatches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         %; Score 720; DB 11;
%; Pred. No. 1.1e-60;
44; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata;
Sciurognathi; Muridae,
                                                                                                                                                                                                                                                        4EB08C81426AEAF1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muridae;
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; Murinae; Mus
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Best Local S
Matches 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMBL/GenBank/DDBJ da.
Respectively. AAH31498.1;
Interpro; IPR002198. ADH_short.
R Interpro; IPR003599; Ig.
R Interpro; IPR003597; Ig_Cl.
R Interpro; IPR003596; Ig_MHC.
R Interpro; IPR003596; Ig_MHC.
R Interpro; IPR003596; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002198; ADH_SI
InterPro; IPR003599; Ig_
InterPro; IPR003597; Ig_c1
InterPro; IPR003596; Ig_wt,
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 2.
SWART; SW00409; IG; 2.
SWART; SW00406; IG; 1.
SWART; SW00406; IG; 1.
  Q91WF8;
01-DEC-2001 (
01-DEC-2001 (
01-MAR-2003 (
Hypothetical
                                                                                                             Q91WF8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8K0F8;
01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8K0F8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 239 AA; 26366 MW; D7BE84398AA341FO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TISSUE-Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                                                                                                                                                                                                  LLQRPGQSPKRLISLVSKLDSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYYCLQSTHFP
                                                                                                                                                                                                                                                                                                                                                                                                                  YQQKPGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGTVKLLIYYTSSLHSGVPSRFSGSGSGTHYSLTISNLEPEDIATYYCQQYSQFPFTFGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTKLEIKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL
  (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
1 25.9 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.4%; Score 702.5; 55.2%; Pred. No. 5.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vert Sciurognathi;
                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                               234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .2e-59;
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                                                                                                                                                   RESULT
OBVC55
ID WC55
ID Q8
AC                       Q
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Best Local S
Matches 132
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Best Local Sin
Matches 136;
                                                                                                                                               Submitted (JAN-2002) to the EMEL: BC021781; AAH21781.1; -.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003396; Ig_v.
Pfam; PF00047; Ig; 2.
Pfam; PF000406; IGv; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; 1.
HypothetLcal protein.
SEQUENCE 239 AA; 26303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                           Q8VC55 PRELIMINARY; PR
Q8VC55;
01-MAR-2002 (TrEMBLrel. 20, Crea
01-MAR-2002 (TrEMBLrel. 23, Last
01-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 26.3 kDa protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001865; Ribosomal_S2.
Pfam; PF00047; 19; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
PROSITE; PS00962; RIBOSOMAL_S2_1; 1.
Hypothetical protein.
SEQUENCE 234 AA; 25929 MW; B0D0B0E6EB7812D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
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[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; I
                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Colon;
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                                                              Local Similarity
mes 132; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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BC015292; AAH15292.1; -
BC015292; APH15292.1; -
Pro; IPR003006; Ig_MHC.
Pro; IPR003996; Ig_v.
Pro; IPR001865; Ribosomal_S2
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MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MMSSAQFLGLLLLCFQGTRCDTQMTQTTSSLSASLGDRVTISCRASQDISNYLNWYQQKP
                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Rođentia;
                                                                                                                                                     26303 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.3%;
58.1%;
                                                                                     57.3%; Score 700.5; DB 11; 55.2%; Pred. No. 8.1e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34;
                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 701; DB 11;
Pred. No. 7.1e-59;
4; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                     C16119CACA25C337
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239
                                                                es 59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64;
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                                                                   Indels
                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS50835; IG_LIKE; 1.
Q91W12;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence up
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation
Unknown (Protein for MGC:6582).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Hypothetical 25.8 kDa protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat
Mummalia; Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q91WS9;
01-DEC-2001
                                                                                                                      Q91W12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                      AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRLLIYD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNGVLNSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSENRNEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLLCFQGSRCDIQMTQTTSSLSASLGDRVTISCSGSQGIANYLNWYQQKPDGTVKLLIYY
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                                                                                                                                                                                                                                       STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    233 AA; 25781 MW; B1C184DA149A16EB CRC64;
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                                                                                                                      PRELIMINARY;
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Pred. No. 7.9e-58;
5; Mismatches 59;
                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
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                                                 sequence update)
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Query Match
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGV; 1.
SWART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 2.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 235 AA; 26021 MW; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9R1A5
Q9R1A5;
01-MAY-2000
                                                                                                                                                                                                                                                                               Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
"Cloning of cDNAs encoding for anti-white pine blister rantibody (Mab 7, its light and heavy chains) and construsingle chain antibody (scFV).";
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF153371; AAD40242.1;
HSSP; P01679; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Kappa light chain of Mab7 (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                     NON_TER
                                                                                                                 SMART; SM00406; IGv; PROSITE; PS50835; IG-PROSITE; PS00290; IG-
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Submitted (APR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                        Pfam; PF00047; ig;
                                                                                                                                                                                                          InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DRFSGSGSGTSYSLTISNMEAEDVATYYCQQWSRNPPTFG/GTKLELKRADAAPTVSIFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                 214
214
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                                                 AA,
                                                                                                                                       IG_LIKE;
                                                 23922 MW;
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  55.3%;
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Pred. No. 1.6e-56;
1; Mismatches 55;
  Score 676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                          lah A.K.M., Misra S.;
anti-white pine blister rust monoclonal
heavy chains) and construction of a
                                                 52BA205FDE995E2A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5FC73BDEBD5E8FEF CRC64;
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RESULT 15
Q8TBC9
ID Q8TBC
AC Q8TBC
DT 01-JU
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Best Local S
Matches 126
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submilted (APR-2002) to the EM EMBL; BC028540; AAR28540.]; -. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v. Pfam; PF00047; ig; 2. SMART; SM00406; IGv; 1. PROSITE; PS00290; IG_MHC; 1. Hypothetical protein. SEQUENCE 234 AA; 25702 MW;
 Q8TBC9;
Q8TBC9;
01-JUN-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 25.7 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Mammary gland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8R028;
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123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       AQLLFLLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAP
                                                                                                                                                                                                                           ELKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWT
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 (TrEMBLrel.
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                                                         PRELIMINARY;
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                   Created)
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Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 655; DB 11;
Pred. No. 1.8e-54;
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7; Mismatches 54;
                                                           PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148377F9C1CD0AEE CRC64;
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Best Local Similarity 43.1%;
Matches 100; Conservative 4:
                                                                                                                                                                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022823; AAH22823.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS00290; IG_MHC; 1.
Hypothetical protein.
Hypothetical protein.
SEQUENCE 233 AA; 24867 MW; 367411BFD6F4DF92 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PISSUE=B-cell;
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                                                                                                                                                                                          LIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQ--QRFNWPWTFGQGTKV 124
                                                      TTPSKQSNNKYAASSYLSLTPEQWKSHKSYSCQVTHEG--STVEKTVAPTEC
                                                                       VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                   LLLPLLTLCTGSEASYELTQ-PPSVSVSPGQTARITCSGDALPKQYAYWYQQKPGQAPVL
                                                                                                                  TVLGQPKAAPSVTLFPPSSEELQANKATLVCLISDFYPGAVTVAWKADSSPVKAG--VET
                                                                                                                                                                           VIYKDNERPSGIPERFSGSSSGTTVTLTISGVQAEDEADYYCQSADSSGTYWVFGGGTKL
                                                                                                                                                                                                                                                               LLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRL
             September
             12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23,
                                                                                                                                                                                                                                                                                            41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation
                                                                                                                                                                                                                                                                                                        Score 458.5; DB 4
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
               13:03:
                                                                                                                                                                                                                                                                                                                       DB 4;
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB B
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length: 2000000000
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    SwissProt_41:*
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Copyright (c) 1993 - 2003 Compugen
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KY1X_HUMAN
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KY1M_HUMAN
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KV3H_HUMAN
KV3M_HUMAN
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KV3B_HUMAN
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                                                                                                                                                                                                                                                                                        KAC_HUMAN
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1109.830 Million cell updates/sec
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homo sapien
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KV3I_HUMAN

ID KV3I_HUMAN

AC P04433;

DT 13-AUG-1987

DT 13-AUG-1987

DT 15-JUL-1999

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OS Homo sapieni
OC Eukaryota; ll
OC Mammalia; El
OX NCBI_TaxID='
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RP SEQUENCE FR

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NYIY_HUMAN	KV1A_HUMAN	KV1S_HUMAN	KV1G_HUMAN	KACB_RAT	KV10_HUMAN	KV30_MOUSE	KV1R_HUMAN	KV1L_HUMAN	KV1E_HUMAN	KV5B_MOUSE	KV1N_HUMAN
	P01593 homo sapien	•	_	٠.	-	_	_		-		•

ALIGNMENTS

P04433;
13-AUG-1987 (Rel. 05, Created)
13-AUG-1987 (Rel. 05, Last sequence update)
13-AUG-1987 (Rel. 05, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
16 kappa chain V-III region VG precursor (Fragment).
17 kappa chain V-III region VG precursor (Fragment).
18 kappa chain V-III region VG precursor (Fragment).
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17 kappa chain V-III region VG precursor (Fragment).
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SEQUENCE FROM N.A. MEDLINE=85087932; NCBI_TaxID=9606;

PubMed=6440122;

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Query Match Best Local Similarity Matches 108; Conser	EMBL; X01668;; NOT_ANNOT PIR; A01900; K3HUVG. HSSP; P80362; LWTL. GO; GO:0005576; C:extracel GO; GO:0005576; C:extracel GO; GO:0006955; P:immune r InterPro; IPR003006; Ig-Vi InterPro; IPR00306; Ig-Vi InterPro; IPR003596; Ig-Vi Pfam; PP00047; Ig; 1. SMART; SM00406; IGV; 1. PROSITE; PS50835; IG_LIKE; Immunoglobulin region; S SIGNAL 1 20 CHAIN 21 >115 DOMAIN 21 >115 DOMAIN 55 69 DOMAIN 77 108 DOMAIN 70 76 DOMAIN 109 115 DOMAIN 115 115 SEQUENCE 115 AA; 12575:	Pech M. Zachau H.G.; Immunoglobulin genes of different subgroups are .nterdigitated within the VK locus."; Nucleic Acids Res. 12:9229-9236(1984). This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usaga by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
46. nilarity 93. Conservative	Y V5 1:337 XX:::	Dachau H.G., Fundament of the VK Locus. Acids Res. 12 Acids Res. 12 SS-PROT entry the Swiss Ir pean Bioinfor non-profit and this star requires a lan email to lan email to
46.4%; 93.9%; ative	68; ; NOT_ANNOTATED_CDS. 0; K3HUVG. 62; INTL. 5576; C:extracellular; NAS. 5576; C:extracellular; NAS. 5576; C:extracellular; NAS. 5576; C:extracellular; NAS. 5695; P:immune response; NAS. 1	n M. Zachau H.G.; numeurowayara, numoglobulin genes of different subgroups a lin the VK locus."; leic Acids Res. 12:9229-9236(1984). leic Acids Res. 12:9229-9236(1984). s SWISS-PROT entry is copyright. It is proceed the Swiss Institute of Bioinformatics European Bioinformatics Institute. There by non-profit institutions as long as by non-profit institutions as long as lified and this statement is not removed. It is requires a license agreement (See httes requires a license agreement (See httes meanil to license@isb-sib.ch).
Score 50 Pred. No 3; Misma		s of different subgroups are interdigitated 2:9229-9236(1984). 2:9229-9236(1984). y is copyright. It is produced through a constitute of Bioinformatics and the EMBL ormatics Institute. There are no restrict institutions as long as its content is attement is not removed. Usage by and for license agreement (See http://www.isb-sib.clicense@isb-sib.ch).
Score 568; DB 1; Pred. No. 3.1e-41; ; Mismatches 4	D_CDS. ar; NAS. ding activity; NAS. ding activity; NAS. onse; NAS. v-III REGION v FRAMEWORK 1. COMPLEMENTARITY-DETERMINING-1 FRAMEWORK 2. COMPLEMENTARITY-DETERMINING-2 FRAMEWORK 3. COMPLEMENTARITY-DETERMINING-3 COMPLEMENTARITY-DETERMINING-3 COMPLEMENTARITY-DETERMINING-3 COMPLEMENTARITY-DETERMINING-3 BY SIMILARITY.). It is pronounce of the conformation of the
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RESULT 2

KV3H_HUMAN

ID KV3H_H

AC P04207

AC Eukary

OC Mammal I

CO MCBI_T

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RN GOIDEI

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CC CHE EU

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SMART; SM00406; IGv;
PROSITE; PS50835; IG.
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01-NOV-1990 (Rel. 16,
15-JUL-1999 (Rel. 38,
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning and sequence determination of a human light-chain gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Goldfien R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jirik F.R., Sorge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-86177570;
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Mammalia; Eutheria; Primates;
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P04207;
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GO:0003823; F:antigen binding a
GO:0006955; P:immune response;
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83.7%;
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region CLL precur
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                                                                             Score 563.5;
Pred. No. 8.5e
8; Mismatches
                                                                                                                                                                 FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
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precursor (Rheumatoid factor).
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g activity;
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RESULT 3

KV3M_HUMAN

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AC P18136

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DT 01-NOV
DT 15-JUL
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P18136;
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J. EXP. Med. 167:840-852(1988).
-I- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
"Autoantibody-associated kappa light chain variable region (
expressed in chronic lymphocytic leukemia with little or no 
mutation. Implications for etiology and immunotherapy.";
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SMART; SM00406; IGv; 1.
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Interpro; IPR003006; Ig_MHC.
Interpro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding act
GO; GO:0006955; P:immune response; NA
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01.NOV-1990 (Rel. 16, Last sequence update
15-JUL-1990 (Rel. 38, Last annotation update)
Ig kappa chain V-III region HIC precursor.
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; P80362; 1WTL.
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Primates;
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85.3%;
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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RESULT 5

KAC_HUMAN STANDARD; PR'
ID KAC_HUMAN STANDARD; PR'
AC P01834;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequent of the seque
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KV3L_HUMAN

ID VX3L_H JL

AC P18135

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T NA MEDLIN

RA MEDLIN

RA MEDLIN

RA WIPS

RT AUTOS

RT EXPES

RT MUTATI

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-i- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN
-i- DISEASE: THE SURFACE IMMUNOGLOBULIN WITH CHRONIC LYMPHOCY
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Eukaryota; Metazoa; Chordata; Craniata
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"Autoantibody-associated kappa light chain variable region expressed in chronic lymphocytic leukemia with little or no mutation. Implications for etiology and immunotherapy.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1
SMART; SM00406; IGV;
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GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NA
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IPR003006;
IPR003596;
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Pred. No. 5.
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COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.

COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
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Olsen K.E., Sletten K., Westermark P.;
"Extended analysis of AL-amyloid protein from abdominal subcutaneous fat biopsy: kappa IV immunoglobulin light c Biochem. Biophys. Res. Commun. 245:713-716(1998).
-!- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOT 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE IIV (1,2)
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MEDLINE-71064023; PubMed-5489770;
Gottlieb P.D., Cunningham B.A., Rut
"The covalent structure of a human acid sequence of the light chain.";
Biochemistry 9:3155-3161(1970).
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(In) Franck F., Shugar D. (eds
Gamma globulins: structure and
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Hieter P.A., Max E.E., Seidman J.G., Maizel J.N.
"Cloned human and mouse kappa immunoglobulin co
genes conserve homology in functional segments.
[c] 22:197-207(1980).
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"Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones proture). IV. The complete amino acid sequence and its significance for the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(197:).
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                                                                                                                                                                                                                                      Biol.
                                                                                                                                                                                                                                   amino acid sequence of a kappa type Bence-Jones protein. lete sequence and the location of the disulfide bridges."; iol. Chem. 244:3550-3560(1969).
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n G.M.;
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PDB; 1D5V; 04-OCT-00.
PDB; 1HEZ; 10-AUG-01.
PDB; 1HKL; 12-MAR-97.
PDB; 117Z; 08-AUG-91.
PDB; 1MIM; 15-MAY-97.
Genew; HGNC: 5716; IGKC.
MIM; 147200;
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01-JAN-1988 (Rel. 06, Last s
15-JUL-1999 (Rel. 38, Last a
19 kappa chain V-III region
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                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MEDLINE-86041852; PubMed-29; Klobeck H.G., Meindl A., Cor "Human immunoglobulin kappa
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                                  SEQUENCE FROM N.A.
                                                        NCBI_TaxID=9606;
                                                                                                                                                P06311;
                                                                                                                                                           KV3K_HUMAN
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SMART; SM00407; IGc1; 1.
PROSITE; PS50835; IG_LIKE; 1.
PROSITE; PS00290; IG_MHC; 1.
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EMBL; V00557;
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InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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Last annotation
region IARC/BL41
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                                                                                                                                     Created)
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            Combriato G.,
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V -> L (IN INV(1,2) MARKER)
/FTId=VAR_003897.
D -> N (IN REF. 7 AND 8).
E -> Q (IN REF. 5 AND 6).
W; 51984D1FDD372CE8 CRC64;
                                                                                                                                                                                                                                                                                                      0;
 light
                                                                                                                                                                                                                                                                                                               Score 548; DB 1;
Pred. No. 1.4e-39;
                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE
                                                                                                                                                           PRT;
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 chain
                                                                                                                          update)
                                                                                                                                                           128
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                                                                                                              update)
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           Solomon
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 of subgroups
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RESULT 7

KV3J_HUM

ID KV3J

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Matches 104
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SEQUENCE
                                                                                                                                      KV3J_HUMAN STANDARD; PRT; 116 AA. P04434; 13-AUG-1987 (Rel. 05, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) 15 kappa chain V-III region VH precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIAM: PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region; S:
                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                       HUMAN
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DOMAIN
  Nucleic
              Pech M., Zachau H.G.;
"Immunoglobulin genes of different subgroups
within the VK locus.";
                                                  SEQUENCE FROM N.A. MEDLINE-85087932;
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0003823; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A01899; K3HU41.
HSSP; P01607; 1REI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                       NCBI_TaxID=9606
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 the VK locus
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FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
JK1 SEGMENT.
BY SIMILARITY.
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Pred.
                                                                                                                Craniata; Vertebrata; Euteleostomi;
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RESULT 8

KV3B_H

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DT 21-JUL

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 PIR; A01892; K3HUSI.
HSSP; P80362; 1WTL.
GO; GO:0005576; C:ext
GO; GO:0003823; F:ant
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SEQUENCE
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                                                                                    group.
                                                                                                          Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable
                                                                                                                                              SEQUENCE
                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat.
Ig kappa chain V-III region SIE.
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                                                                         Biochemistry 20:5816-5822(1981)
                                                                                                                                 MEDLINE=82046598; PubMed=6794615;
                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                          Homo sapiens (Human)
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InterPro; IPR003006; Ig_MHC.
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                                                MISCELLANEOUS: THIS GLOBULIN ACTIVITY.
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 C:extracellular; F:antigen binding
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FRAMEWORK-1
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig kappa Chain V-III region Ti.
Homo sapiens (Human).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                  the mechanism of antibody production.";
Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972)
-i- MISCELLANEOUS: THE C. REGION OF THIS CHAIN HAS
-i- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                 Suter L., Barnikol H.U., Watanabe S., Hilschmann N.; "Rule of antibody structure. The primary Structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones prot Ti). IV. The complete amino acid sequence and its significance for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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HSSP; P80362; 1WTL.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                  Immunoglobulin V region; Bence-Jones protein.
DISULFID 23 89 BY SIMILARITY.
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GO:0003823; F:antigen binding activ
GO:0006955; P:immune response; NAS
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                                                                                        Similarity
                        DRESGSGSGTDETLTISRLEPDDEAVYYCQQYGSSPQTEG JGSKVEIKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EIVLTQSPATLSLSPGERATLACRASQTASR-YLAWYQQK?GQAPRLLIYDTSNRATGIP
ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ETVLTQSPGTLSLSPGERATLSCRASQSVSNSYLAWYQQK?GQAPRLLIYGASSRATGIP
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109
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11775 MW;
                                                                                                                             11788 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.7%;
81.7%;
                                                                                      36.7%;
82.6%;
                                                                                      Score 448.5; DB 1;
Pred. No. 3.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 448.5; DB 1
Pred. No. 3.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ВY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                            8C35058CDC7749BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7689C3ECD646FFB4 C3C64;
                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
                                                                                                                                                                                                                                                                   activity; NAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAS
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                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                   (Bence-Jones protein significance for
                                                                                                  Length
                                                                                                                                                                                                                                                                                                                               THE
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                               INV (3) MARKER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                    109;
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                                                                          <u>ب</u>
                                                                          Gaps
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RESULT 10

KV3F_HUMAN

ID

VV3F_H
AC

P01624

DT 21-JUL

DT 21-JUL

DT 16-OCT

DE IG kapp
OS HOMO S

OC Mammal

OX NCBI_T

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CC -1- MI

CC -1- MI

CC -1- MI

CC GO; GC

DR PIR; #

DR Inter:
DR Inter:
DR Inter:
DR PROSIT

KW IMMUNC

KW IMMUNC

FT NON_TI

SQ SEQUEI
RESULT 11

KV3E_HUMAN

ID KV3E_H

AC P01623

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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ### PF00047; 19; 1.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region.

DISULFID 23 89

NON_TER 109 109

SEQUENCE 109 AA; 11922 MW;
                                                                                                     Ig kappa chain
Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KV3F_HUMAN
P01624;
    Andrews D.W., Capra J.D.;
Andrews D.W., Capra J.D.;
"Amino acid sequence of the variable regions of light chains
"Amino acid sequence of the variable regions of light chains
                                                                                                                                                          21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation updat
Ig kappa chain V-III region WOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-76276460; PubMed-60899;
Klapper D.G., Capra J.D.;
"The amino acid sequence of the variable regions of t from two idiotypically cross reactive IgM anti-gamma Ann. Immunol. (Paris) 127C:261-271(1976).
-1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IC GLOBULIN ACTIVITY.
BIR; A01897; K3HUPM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
1g kappa chain V-III region POM.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                    KV3E_HUMAN
P01623;
                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                           EDLINE=82046598;
                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activ GO:0006955; P:immune response; NAS. erro; IPR007110; Ig-like. erro; IPR003006; Ig_MHC. erro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P80362;
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                                                                                                                                                                                                                                                                                                                                                                                                                       96;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                     ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKR 128
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1WTL.
                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                           PubMed=6794615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11922 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  36.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                    9;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 442.5;
Pred. No. 1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                  Catarrhini;
                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62821DDC6A8ABA86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      activity;
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                                                                                                                                                                         update)
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                                                                                                                  Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the light chains
                                                                                                                    Homo
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                of the
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              from two of the Wa
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KV3G_HUMAN
Query Match
Best Local S
Matches 88
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Best Local
                                                                                                                                                     InterPro; IPR007110; Ig-11Ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003966; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PR0SITE; PSS0835; IG_LIKE; 1.
Immunoglobulin V region.
                                                                                      DISULFID
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                          MEDLINE-86230578; PubMed-3086710;
Mewkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Mewkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Mewkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Mewkirk M., Chen P.P., Carson D.A., Posnett D., Capra J.D.;
Teactivity with antipeptide antibodies.";
mol. Immunol. 23:239-244(1986).
PIR; A01893; K3HUGO.
MSSP, P80362; 1WTL.
GO: GO:0005576; C:extracellular; NAS.
GO: GO:0005825; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P04206;
20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 Appa chain V-III region GOL (Rheumatold fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005576; C:extracellular; NAS: GO; GO:0003823; F:antigen binding act GO; GO:0006955; P:immune response; NF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A01896; K3HUWL. HSSP; P80362; 1WTL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biochemistry 20:5816-5822(1981)
-!- MISCELLANEOUS: THIS CHAIN W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KV3G_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLOBULIN ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80
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  88;
                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIVLTQSPATLSLSPGERATLACRASQT-ASRYLAWYQQKPGQAPRLLIYDTSNRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EIVLTQSPGTLSLSPGERATLSCRASQSVSSGYLGWYQQKPGQAPRLLIYGASSRATGIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                      109 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                109 AA;
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  Conservative
                                                                                                           23
109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata; (
                                                                                        11830 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11746 MW;
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81.7%;
                    36.1%;
Score 441.5;
Pred. No. 1.3e
8; Mismatches
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8;
                                                                                                                                    ВY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 441.5;
Pred. No. 1.3
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                                                                                        9349A5B1D93588B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                566C115E6B9CBEEE CRC64;
                                                                                                                                    SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activity;
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                       .3e-30;
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                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor)
  12;
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  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
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1;
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Gaps
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21

EIVLTQSPATLSLSPGERATLACRASQTASR-YLAWYQQKPGQAPRLLIYDTSNRATGIP

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RESULT 13

KV4C_HUMAN

ID 4C_HUMAN

ID 701-JAPR

DT 01-JAPR

DT 01-JAPR

DT 01-APR

OC Mammal

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                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00047; 19; 1.
SMART; SM00406; IGv;
PROSITE; PS50835; IG_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR0071110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1988 (Rel. 05, Created)
01-APR-1988 (Rel. 07, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
15 kappa chain V-IV region B17 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marsh P., Mills F., Gould H.;
"Detection of a unique human V kappa cDNA probe.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=86041854; PubMed=2997713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KV4C_HUMAN P06314;
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVISION TO
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                                                                                                                                                                                                                                                                                                                                                                                                                     [mmunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             X02990; CAA26733.1; -. P80362; LWTL.
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acids Res.
                     MEAPAQULFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTA-----SRYLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Gv; 1.
IG_LIKE; 1.
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                                                                                                                                                                     14966
                                                                                                       35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Signal
                                                                                                                                                                   MW;
                                                                                 Pred. No. 1.10
17; Mismatches
                                                                                                    Score 432;
Pred. No. 1
                                                                                                                                                                                                         FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3
FRAMEWORK-4.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                       FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2
                                                                                                                                                                                                                                                                                                                               IG KAPPA CHAIN V-IV REGION B17 FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                 6413A22FD0738832 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity;
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                                                                                 DB 1;
1.1e-29;
hes 28;
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                                                                                                                      Length 134;
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RESULT 14

KV3A_HMAN

ID KV3A_H

ID KV3A_H

P01619

P1 21-JUL

P1 21-JUL

P1 15-JUL

RN (1)

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Best Local
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                                                                                                                                                                                                                                   P06310;
Ol-JAN-1988 (Rel. 06, Created)
Ol-JAN-1988 (Rel. 06, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
If kappa chain V-II region RPMI 6410 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
Ig kappa chain V-III region B6.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KV3A_HUMAN
P01619;
                                   SEQUENCE FROM N.A.
MEDLINE-86041852; PubMed-2997711;
Klobeck H.G., Meindl A., Combriato G., Seriona immunoglobulin kappa light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMNOTIE; PS50835; IG_LIKE; 1.
Immunoglobulin v region; Bence-Jones protein.
DISULFID 23 89 BY SIMILARITY.
NON_TER 108 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The basic sequences of immunoglobulin kappa of Bence Jones proteins Rad, Fr4 and B6.";
                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrati; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominid:1e; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A01891; K3HUB6.
Nucleic
                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                KV2F_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Milstein C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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13:6499-6513(1985)
                                                                                                                                                                             Chordata;
Primates;
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75.0%;
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Ig_MHC.
Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 427.5; DB 1
Pred. No. 1.9e-29;
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                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                PRT;
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Best Local S
Matches 78
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PIR; A01890; K2HURP.
HSSP; P80362; HWTL.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0005576; C:extracellular; NAS.

G0; G0:0003823; F:antigen binding activity; NAS.

G0; G0:0006955; P:immune response; NAS.

InterPro; IPR0077110; Ig-1ike.

InterPro; IPR00306; Ig-NHC.

InterPro; IPR00396; Ig-WHC.
                                                                                                                                                                                                                                                                                Pfam; PF00047; 1g; 1.

SMART; SM0406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Signal.

SIGNAL 1 20

CHAIN 21 133 IG KA

DOMAIN 21 43 FRAME

DOMAIN 44 59 COMPL

DOMAIN 60 74 FRAME

DOMAIN 75 81 COMPL

DOMAIN 82 113 FRAME

DOMAIN 82 113 FRAME

DOMAIN 114 122 COMPL

DOMAIN 114 122 FRAME

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DOMAIN 114 122 FRAME

DOMAIN 114 122 FRAME
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SEQUENCE
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116 WTFGQGTKVEFKR 128
|||||||||||
|121 WTFGQGTKVEIKR 133
                                                            61
                                                                          Similarity
                                                          FQQRPGQSPRRLIYKVSNRDSGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQGTHWS 120
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AA;
                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                          14707 MW;
                                                                                                                                                                             35.0%; Score 427.5; DB 1; 58.6%; Pred. No. 2.5e-29; Live 24; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                        IG KAPPA CHAIN V-II REGION RPMI 6410. FRAMEWORK-1. COMPLEMENTARITY-DETERMINING-1.
                                                                                                                                                                                                                                                                                  COMPLEMENTARITY-DETERMINING-3. FRAMEWORK-4.
                                                                                                                                                                                                                                                                                                                          FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
                                                                                                                                                                                                                                                                      BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                 FRAMEWORK - 3
                                                                                                                                                                                                                                        513CCAF3673009EE CRC64;
                                                                                                                                                                                                           DB 1; Length 133;
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Search completed: September 12, 2003, 13:01:16 Job time: 10.9153 secs

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Minimum DB
Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein A;Residues: 1-215 <ALI> G;Residues: 1-215 <ALI> C;Superfamily: immunoglobulin V region; immunoglobulin F;16-91/Domain: immunoglobulin homology <IMM>
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Ig kappa chain – h	Ig kappa chain pre	Ig kappa chain V r	Ig lambda-like cha	Ig kappa chain V r	Ig kappa chain C r	anti-Sm antibody V	Ig kappa chain pre	Ig kappa chain - h	Ig kappa chain pre	Ig kappa chain pre	Ig kappa chain V-J	Ig kappa chain pre	Ig kappa chain V-J	Ig kappa chain (WM	Ig kappa chain V r

ALIGNMENTS

05-Dec-1998

#te::t_change

21-Jan-2000

kappatype

Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

light chains with AL amyloidosis:

homology

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RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C.Species: Homo sapiens (man)

C.Species: Homo sapiens (man)

C.C.Accession: JE0244

R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, S.; Kazi, submitted to JIPID, November 1998

submitted to JIPID, November 1998

submitted to JIPID, November 1998
                                      A;Description: A new subgroup of k type light chains (VkV) identified A;Reference number: JE0243
A;Recession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region;
F;16-90/Domain: immunoglobulin homology
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91.6%;
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Pred. No. 1.1e-62;
4; Mismatches 13;
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<IMM>
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ΑL

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Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 2
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A;Molecule type: protein
A;Residues: 1-215 <LEO>
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JEO243

JEO243

Ig kappa chain NIG93 precursor - human

C. species: Homo sapiens (man)

C. pate: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change

C. Accession: JEO243

R.Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.;

submitted to JIPID, November 1998

A. Description: A new subgroup of k type light chains (VkV) ident
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Pred. No. 5e-
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Ig kappa chain Am37 precursor - human
C; Species: Homo sapiens (man)
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-C; C; Cacession: JE0241
R; Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takeda K; Takeda K; Kojima, M.; Takeda K; Ig kappa chain precursor - rat (Species: Rattus norvegicus (Norway rat) C; Species: Rattus norvegicus (Norway rat) C; Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change C; Accession: S06084 R; Crowe, J.S.; Smith, M.A.; Cooper, H.J. Nucleic Acids Res. 17, 7992, 1989 A;Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunog A;Reference number: S06084; MUID:90016888; PMID:2508067
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89.7%;
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6; Mismatches
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Pred. No. 1.6e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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RESULT 7

S01320

Ig kappa chain precursor - mouse
C; Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C; Accession: S01320
R; de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Bur. J. Biochem. 176, 287-295, 1988
A; Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed A; Reference number: S01320; MUID:88329081; pMID:3138116
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A; Molecule type: mRNA
A; Residues: 1-240 <CRO>
A; Residues: 1-240 <CRO>
A; Cross references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
A; Cross references: EMBL:X16129; Immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-240/Product: Ig kappa chain #status predicted <MAT>
F;153-222/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-234 <DE1>
A;Cross-references: EMBL:x13187; NID:g51784; PIDN:CAA31579.1; PID:g51785
A;Cross-references: EMBL:x13187; NID:g51784; PIDN:CAA31579.1; PID:g51785
A;Note: this sequence was determined from the differentiated gene
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                     F;1-20/Domain: signal sequence #status predicted <SIG>F;21-234/Product: Ig kappa chain #status predicted <MAF;36-110/Domain: immunoglobulin homology <IMM>
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                                                                                                                                             PWTFGQGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNAL 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WYQQKPGQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRENW 114
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                                                                                                                                                                                                 GKSPQLLVYVATKLVDGVPSRFSGSGSGTQYSLKINSLQSEDFGSYYCQHFWDTPFTFGS
                                                                                                                                                                                                                                   GQAPRILIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                                                                                                                                                                                                                                          MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP 60
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                                                 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC
                                                                                                                        GTKLEMKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVL
                                                                                                                                                                                                                                                                        MSVPTQVLGLLLLWLTDARCDIQMTQSPASLSVSVGESVTITCRASENIYSNLAWYQQKQ
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                                                                                                                                                                                                                                                                                                                                             Score 727; DB 2;
Pred. No. 3.5e-43;
7; Mismatches 62
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Pred. No. 3.4e-46;
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A;Accession: S33161
A;Status: preliminary
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A; Residues: 1-234 <VAN>
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136; Conserv
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56.8%;
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A; Molecule type: mRNA
A; Residues: 1-230 <FOL>
A; Cross-references: EMBL:X54110; NID:g297103; PIDN:CA#38046.1; PID:g1364221
C; Superfamily: immunoglobulin V region; immunoglobulir homology
C; Keywords: heterotetramer; immunoglobulin
F;143-212/Domain: immunoglobulin homology <IMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig kappa chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (dcmestic sheep)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-
C:Accession: S33161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D. Eur. J. Blochem. 192, 767-775, 1990
A;Title: Construction and characterization of a recombinant murine monoclonal antibo A;Reference number: S14236; MUID:91006173; PMID:2209622
A;Accession: S14237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Foley, R.C.; Beh, K.J. submitted to the EMBL Data Library, July 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig kappa chain precursor (15C5) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: S14237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 NSWTDQDSKDSTYSMSSTLTLTKDEYERHNSYTCEATHK1STSPIVKSFNRNEC 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GKSPKTLIYRGNRLVAGVPSRFSGSGSGQDYSLTISSLEYEDVGVYYCLRYDEFPFTFGS
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                                                                                                                          61 KLLIYYATRLHTDVPSRFSGSGSGTDYTLTISNLEANDTFTYYCLQYESTPLAFGGGTNV
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EIKRSDAQPSVFLFKPSEEQLRTGTVSVVCLVNDFYPKDINVKVKVDGVTQNSNFQNSFT
                                                                                                                                                 RLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDF&VYYCQQRFNWPWTFGQGTKV
                                                                                                                                                                                                                                              QLLGLLLLMLLPGARCDIQVTQSPSSLSASLTERVSITCFTSQSVSNYLNWYQQKPGQAP
                                                                                                                                                                                                                                                                           QLLFLLLLW-LPDTTGEIVLTQSPATLSLSPGERATLACFASQTASRYLAWYQQKPGQAP
                                                          EFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREPKVQWKVDNALQSGNSQESVT 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MRTPAQFLGILLLWFPGIKCDIKMTQSPSSMYASLGERVTVTCKASQDINSYLSWIQQKP
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                                                                                                                                                                                                                                                                                                                                                                   57.5%; Score 703.5; DB 2
59.1%; Pred. No. 1.4e-41;
tive 35; Mismatches 58
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Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision
C;Accession: $37484
R;Ducancel, F.F.D.
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C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired
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A; Residues: 1-225 <DUC>
A; Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A; Residues: 1-219 < KIP>.
A; Cross-references: EMBL: 227396; NID: g416538; PIDN: CAA81787.1; PID: g416539
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
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A; Accession: S38865
A; Status: preliminary
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A; Status: preliminary
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                                 TSNRATGIPARESGSGSGTDETLSISSLEPEDEAVYYCQQRENWPWTFGQGTKVEFKRTV 130
                                                                                               LLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKPGQAPRLLIYD
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59.88;
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58.9%;
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'
                                                                                                                                            Score 702.5; DB 2
Pred. No. 1.6e-41;
7; Mismatches 54
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Pred. No. 1.6
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C;Comment: This catalytic antibody has peroxidase oxidase. It is directed C;Superfamily: immunoglobulin V region; immunoglobulin homology E;16-94/Domain: immunoglobulin homology IMM>
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A; Title: Structural A; Reference number: A; Accession: JC5810
                                                                               R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguc Biochem. Biophys. Res. Commun. 240, 566-572, 1997 A;Title: Structural characterization of mouse monoclonal A;Reference number: JC5810; MUID:98063277; PMID:9398605
                                                                                                                                                                                              monoclonal antibody 13-1 light chain - mouse
C;Speckes: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: JC5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:D29670
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross references: EMBL:D29670; NID:g473962; PIDN:BAA06141.1; PID:g473963
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyr A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68214
A;Status: nucleic acid sequence not shown
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N;Alternate names: immunoglobulin light chain
C;Species: Mus musculus (house mouse)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change
C;Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.;
submitted to the EMBL Data Library, March 1994
A;Description: Specific peroxidase activity by formation of an a
A;Reference number: S68241
A;Accession: S68241
A; Molecule type: protein A; Residues: 1-218 < AKA>
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A; Residues: 'NI', 3-212 <TAW>
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A; Residues: 1-218 <TAK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 GIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSVF 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 EIVLTQSPATLSLSPGERATLACRASQTASR----YLAWYQQKPGQAPRLLIYDTSNRAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVPARFSGSGSGTDFTLNIHPVEEEDVATYYCQHSRELPLTFGAGTKLELKRADAAPTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLATNLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAPSVFTFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%;
61.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 702; DB 2;
Pred. No. 1.7e-41;
2; Mismatches 49
                                                                                                                                                                      Yamaguchi, H.; Kamachi, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234
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                                                                                                                                                                         Harada,
                                                                                                                  porp
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against a

Matches

Conservative

30; Mismatches

Query Match Best Local Similarity

56.9%;

Score 696; DB 2; Pred. No. 4.4e-41;

Length 218

Indels

Gaps

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Ig kappa chain precursor V-J-C region (LS1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0106
C;Accession: PL0106
C;Accession: PL0106
R;Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A;Title: Relationship of variable region genes expressed by a human B cell lymphoma secrification of the secretary of the
Ig kappa chain V region (17/9) - mouse (Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000 C;Accession: A31790 R;Schulze-Galmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; W J. Biol. Chem. 263, 17100-17105, 1988 A;Title: Preliminary crystallographic data, primary sequence, and binding d: A;Reference number: A92686; MUID:89034213; PMID:3182835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                          198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22 IVLTQSPATLSLSPGERATLACRASQTASR----YLAWYQQKPGQAPRLLIYDTSNRATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 IPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQGTKVEFKRTVAAPSVFI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MEAPAQLLFLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSWTDQDSKDSTYSMSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GQAPRLLIYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQQRSNWPLTFGG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEAPAQLLELLLIMLPDTTGEIVLTQSPATLSLSPGERATLSCRASQSVSSYLAWYQQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVLTQSPASLAVSLGQRATISCRASKSVSASGYIYMHWYQQKPGQPPKLLISLASNLESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 695; DB 2;
Pred. No. 3.4e-41;
4; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                       Kenten, J.H.; Wilson,
                                      and binding data for an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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A;Accession: A31790
A;Mclecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:C;Superfamily: immunoglobulin V region; immunoglobulin C;Reywords: heterotetramer; immunoglobulin F:16-96/Domain: immunoglobulin homology <IMM>
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181
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                                                                                   135 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALCSGNSQESVTEQDSKDSTYS 194
                                                                                                                                                                                                                                                                              128;
                                                                                                                                      75 ATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRENWIWTFGQGTKVEFKRTVAAPS 134
                                                                                                                                                                                                                                         21 EIVLTQSPATLSLSPGERATLACRASQT-----ASRYLAWYQQKPGQAPRLLIYDTSNR 74
                                                                                                                                                                                                         1 DIVMTQSPSSLTVTAGEKVTMSCTSSQSLFNSGKQKNYLTWYQQKPGQPPKVLIYWASTR 60
                                                                                                                                                                                                                                                                                              Similarity
MSSTLTLTKDEYERHNSYTCEATHKTSTSPIVKSFNRNEC 220
                              LSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                                   VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEFQNGVLNSWTDQDSKDSTYS
                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                         56.8%;
58.2%;
                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                          Score 695; DB 2;
Pred. No. 5.3e-41;
38; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                            1; NID:g533234; immunoglobulin
                                                                                                                                                                                                                                                                              48;
                                                                                                                                                                                                                                                                                                              Length 220
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Search completed: September 12, 2003, 13:04:26 Job time: 18.5169 secs

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Result
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      2196
2193.5
2193.5
2187
2183
2183
2183
      2181.5
2181.5
2181.5
2181.5
                                                                                                                                                                         2257
2249.5
                                                                                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                           Match
        100.0
100.0
90.7
99.8
89.8
89.4
87.4
87.4
87.3
87.3
87.3
86.8
86.8
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2514
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                                                                                                                                                                                                                                                                                            Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published_Applications_AA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                      : /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                              DB
 US-10-225-108A-3
US-09-848-832-3
US-09-948-832-3
US-09-948-26-98A-26
US-10-150-475A-6
US-10-227-694-5
US-10-227-694-5
US-09-726-258-71
US-09-726-258-71
US-09-948-429B-8
US-10-124-807-8
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2245.783 Million cell updates/sec
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Sequence 3, Appli
Sequence 21, Appli
Sequence 26, Appli
Sequence 6, Appli
Sequence 9, Appli
Sequence 9, Appli
Sequence 71, Appli
Sequence 11, Appli
Sequence 8, Appli
Sequence 8, Appli
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ALIGNMENTS

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US-10-225-108A-3

Sequence 3, Application US/10225108A

Publication No. US20030157112A1

GENERAL INFORMATION:

APPLICANN: HOOPER, Craig

APPLICANN: HOOPER, Craig

APPLICANN: DIFT2SCHOLD, Bernhard

APPLICANN: DIFT2SCHOLD, Bernhard

FILLE OF INVENTION: and Methods for Making Them

FILLE OF INVENTION: and Methods for Making Them

FILLE APPLICATION NUMBER: US/10/225,108A

CURRENT APPLICATION NUMBER: US 60/304-10

CURRENT FILLING DATE: 2003-04-10

PRIOR APPLICATION NUMBER: US 60/204,518

PRIOR APPLICATION NUMBER: US 60/204,518

PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR FILLING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR FILLING DATE: 2001-08-21

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PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR FILLING DATE: 2001-08-21

PRIOR POLICATION NUMBER: US 60/314,023

PRIOR FILLING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/314,023

PRIOR FILLING DATE: 2001-08-21

PRIOR APPLICATION NUMBER: US 60/314,023

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; TYPE: PRT
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CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/204,518
PRIOR FILING DATE: 2000-05-16
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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Best Local
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KFNWYYDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
                                         VTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDK 240
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Pred. No. 3.4e-165;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/736,371B
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 9815909.8
PRIOR FILING DATE: 1998-07-21
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR APPLICATION NUMBER: PCT/GB99/02380
PRIOR FILING DATE: 1999-07-21
NUMBER OF SEO ID NOS: 30
SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 21
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Sequence 21, Application U. Patent No. US2002013196BA1
GENERAL INFORMATION:
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ORGANISM: Homo
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                                                                      DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
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                                                                                                              PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
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Pred. No. 4.7e-149;
B; Mismatches 11;
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                                                                                        Sequence 6, Application US/10150475A
Publication No. US20030103985A1
GENERAL INFORMATION:
APPLICANT: Adolf, G. et al.
TITLE OF INVENTION: Cytotoxic CD44 Antibody
FILE REFERENCE: 1/1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/538,913
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Microsoft Word
SEQ ID NO 26
CURRENT APPLICATION NUMBER: US/10/150,475A CURRENT FILING DATE: 2002-05-17 PATOR APPLICATION NUMBER: US 60/307,451 PRIOR FILING DATE: 2001-07-24 NUMBER OF SEQ ID NOS: 9 SOCTWARE: PAtentin Ver. 2.1 SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity
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APPLICANT: Henderikx, Maria P.G.
TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
FILE REFERENCE: DXX-015.1 US
CURRENT APPLICATION NUMBER: US/09/822,698A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 451
TYPE: PRT
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                                                                                                                                                                                                                         413
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                                                                                                                                                                                                                                                                                                                       KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                             QGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                      KLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                                                                                                                                                                       QGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKH-----TGGGVWDPIDYWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89.8%;
93.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 2257; DB IV;
Pred. No. 1.6e-147;
                                                                                                    Immunoconjugates
                                                                                                                                                                                                                      451
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; OTHER INFORMATION:
; OTHER INFORMATION:
US-10-150-475A-6
                                                           ; OTHER INFORMATION: US-10-020-786-9
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Query Match
Best Local Similarity
Matches 418; Conserv
                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/10020786 Publication No. US20030073164A1
                                                                                                                                                SEQ ID NO 9
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Best Local Similarity
                                                                                                                                                                                                                                 APPLICANT: Simmons, Laura C.
APPLICANT: Klimowski, Laura
APPLICANT: Reilly, Dorothea
APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/020,786
CURRENT FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
                                                                                                    ORGANISM: Artificial sequence
                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                          DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKITPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPPCPAP 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPE?VTVSWNSGALTSGVHTFPA
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                                                                       anti-TF heavy chain
             87.4%;
88.6%;
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92.7%;
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Score 2196;
Pred. No. 2.
9; Mismatche
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 ; DB 15;
2.6e-143;
hes 37;
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                           Length
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                              470;
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Conservative

Mismatches

Indels

8;

Gaps

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US-10-227-694-5
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                                                                                                                                                                                                                                                                                         US-10-227-694-5
                                                                                                                                                                                                                                                                                                                                             APPLICANT: Simmons, Laura
APPLICANT: Andersen, Dana
TITLE OF INVENTION: A SYSTEM FOR ANTIBODY EXPRESSION AND ASSEMBLY
FILE REFERENCE: p1867R1
CURRENT PPLICATION NUMBER: US/10/227,694
CURRENT FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: US 60/315,209
PRIOR FILING DATE: 2001-08-27
NUMBER OF SEQ ID NOS: 6
SEQ ID NO 5
LENGTH: 470
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/10227694 Publication No. US20030077739A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                            Local Similarity
                 183
                                              127
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                                           MIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 182
------FDYWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 178
              VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
                                                                                                                     GLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVT
                                                                                                                                                                                FGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGK 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIVVLNGGFDYMGOGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
|------FDYMGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT
                                                                                                       GLEWYGLIDPEQGNTIYDPKFQDRATISADNSKNTAYLQMNSLRAEDTAVYYCARDTAAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLEWVGLIDPEQGNTIYDPKFQDRATISADNSKNTAYLQMNSLRAEDTAVYYCARDTAAY 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVT
                                                                                                                                                                 FLLASMFVFSIATNAYAEVQLVESGGGLVQPGGSLRLSCAASGFNIKEYYMHWVRQAPGK
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ISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                          87.4%;
                                                                                                                                                                                                                            Score 2196; DB 15;
pred. No. 2.6e-143;
9; Mismatches 37;
                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                        470;
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                                                                                                                                                                                                                            Gaps
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                                                                       ; TYPE: Am;
; TOPOLOGY:
US-09-726-258-71
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US-09-726-258-71
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                                                                                                    TELEFAX: 650/32... 71.
INFORMATION FOR SEQ ID NO: 71.
SEQUENCE CHARACTERISTICS:
FENGTH: 452 amino acids
         Query Match
Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 71, Application US/09726258 Publication No. US20030021790A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Genentech, Inc., Hsel, Vanessa
APPLICANT: Koumenis, Iphigenia
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES
                                                                                                                                                                               REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5530
                                                                                                                                                                                                                         APPLICATION NUMBER: 60/09
FILING DATE: 24-JUL-1998
ATTORNEY/AGENT INFORMATION:
NAME: LOVE, Richard B.
REGISTRATION NUMBER: 34.6
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WinPatin (Ge
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   FILING DATE:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKV
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               Conservative
                                                                                       Linear
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                          87.3%;
91.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                      (Genentech)
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                                                                                                                                                                                                                                                                                                                                   09/234,182
                                                                                                                                                                                                                         34,659
                                                                                                                                                    71:
          Score 2193.5;
Pred. No. 3.7e.
9; Mismatches
               9;
                                                                                                                                                                                                              P1085R4-1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  floppy
                             .7e-1
                                           DB 11;
                                          Length
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               Gaps
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RESULT 9
US-10-020-786-11
                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: US-10-020-786-11
                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 11
LENGTH: 476
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10020786 Publication No. US20030073164A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/256,164
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/020,786 CURRENT FILING DATE: 2002-03-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Yansura, Daniel G.
TITLE OF INVENTION: PROKARYOTICALLY PRODUCED ANTIBODIES AND USES THEREOF
FILE REFERENCE: P1793R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Simmons, Laura C. APPLICANT: Klimowski, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
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                                                                                                      GLEWVSAISA-SGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREV
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                                                                                   GLEWVGWINTYTGEPTYAAD-FKRRFTFSLDTSKSTAYLQMNSLRAEDTAVYYCAK--YP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                       anti-VEGF heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-03-26
                                                                                                                                                                                                                   87.0%; Score 2187; DB 15; 88.8%; Pred. No. 1.1e-142; tive 14; Mismatches 35;
                                                                                                                                                                                                                     Indels
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US-09-948-429B-8
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                                Query Match
Best Local S
Matches 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION: APPLICANT: Anders
                                                                                                                                                                                                    TELEPHONE: 703-836-66:
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                               Local Similarity 86.7 nes 418; Conservative
                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L
REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 699 Prin
CITY: Alexandria
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699 Prince Street
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                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BURNS,
                                                                                                                                                                                                                                      703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                protein
                                              86.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEE
IMMUNOSUPPRESANTS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOANE, SWECKER & MATHIS
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                                                                                                                                                                                                                                                                                     35,030
                                                                                                                                                                                                     80
                                18;
                                                                                                                                                                                                                                                                      012712-131
                                Score 2183; DB 10;
Pred. No. 2.1e-142;
8; Mismatches 34;
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                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Anderson, Darrell R.

TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FO TITLE OF INVENTION: PHARMACEUTIAL COMPOSITIONS CONTAINING, TITLE OF INVENTION: IMMUNOSUPPRESANTS"

NUMBER OF SEQUENCES: 12
                                                   APPLICATION NUMBER: US 00 FILING DATE: 07-JUN-1995 ATTORNEY/ACENT INFORMATION:
                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                         STREET: 699 Prince
CITY: Alexandria
STATE: VA
COUNTRY: USA
COUNTRY: 2314
                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
NAME: TESKIN, ROBIN L.

REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01
ELECOMMUNICATION INFORMATION:
                                                                                                                                     CLASSIFICATION:
                                                                                                                                                     FILING DATE:
                                                                                                                                                                 APPLICATION NUMBER:
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                                                                                US 08/487,550
                                                                                                                                                                US/10/124,807
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US-10-124-905-8
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APPLICANT: Anderson,
TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF INVENTION: ITTLE OF SEQUENCES:
                                                                                                                                                                                                                                            Sequence 8, Application US/10124905 Publication No. US20020166136A1
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Best Local Similarity
Matches 418; Conserv
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SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
TYPE: amino acid
         ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                             CITY:
STATE:
                                                                               STREET: 655
CITY: Alexandria
                                                                 COUNTRY:
OPERATING SYSTEM:
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                                                                                                                                                                                                                  Anderson,
                                                                  USA
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            compatible
                                                                                                                                                                       , Darrell R.

"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEI
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86.7%;
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 PC-DOS/MS-DOS
                                                                                                         Street
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                                                                                                                       SWECKER &
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Pred. No. 2.
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2.1e-142;
nes 34;
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-10-124-905-8
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Best Local Sim
Matches 418;
Sequence 2, Application US/10356974
Publication No. US20030153735A1
GENERAL INFORMATION:
APPLICANT: BREECE, TIMOTHY N.
APPLICANT: FAHRNER, ROBERT L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/487,550 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Teskin, Robin L. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                       APPLICANT: BASEY, CAROL D.
APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/10/253,366
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US/09/304,465
PRIOR PILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
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                          SEQ ID NO 2
  TYPE: PRT
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US-10-356-974-2
                                                    US-10-253-366-2
                                                                    RESULT 14
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APPLICANT: PENG, DAVID
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1939R1
CURRENT APPLICATION NUMBER: US/10/356,974
CURRENT FILING DATE: 2003-02-03
PRIOR APPLICATION NUMBER: US 60/354,579
PRIOR FILING DATE: 2002-02-05
PRIOR FILING DATE: 2002-02-05
Sequence 2, Application US/10253366 Publication No. US20030078388A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 2
LENGTH: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 416;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial sequence
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                                                                                                                        411
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                                                                                                                                                                                                                                                            PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS:#EDPEVKFNWYVDGVEVHNA
                                                                                                                                                                                                                                                                                                                                                                                                    HTFPAVLQSSGLYSLSSVYTVPSSSLGTQTYICNVNHKPSJTKVDKKVEPKSCDKTHTCP
                                                                                                                        SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                         SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473
                                                                                                                                                                                         VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
                                                                                                                                                                                                             VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDR SVTMIVVLNGG-----FDYW 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQA?GKGLEWVARIYPTNGYTRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Pred. No. 2.4e-142;
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; OTHER INFORMATION: Sequence is US-10-253-366-2
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                                                                                                                               ; OTHER INFORMATION: US-10-316-694-2
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US-10-316-694-2
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Publication No. US20030118583A1
GENERAL INFORMATION:
APPLICANT: EMERY, JEFFERSON C.
APPLICANT: MCDONALD, PAUL J.
APPLICANT: O'LEARY, RHONA M.
TITLE OF INVENTION: STABILIZING POLYPEPTIDES WHICH HAVE BEEN EXPOSED TO UREA FILE REFERENCE: p1940R1
CURRENT APPLICATION NUMBER: US/10/316,694
CURRENT PILING DATE: 2002-12-11
PRIOR APPLICATION NUMBER: US 60/341,891
PRIOR FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                          SEQ ID NO 2
LENGTH: 449
TYPE: PRI
ORGANISM: Artificial sequence
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Best Local Similarity
Matches 416; Conserval
                                                                   Matches
                                                                                                Query Match
                                                                                                                                                                FEATURE:
                                                                                 Local
                                                                   416;
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                20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAPGKGLEWVSAISASGHSTYL 79
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                                                                h 86.8%;
Similarity 90.6%;
16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 434
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EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLEWVARIYPTNGYTRY 60
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Pred. No. 2.4e-142;
8; Mismatches 20; Indels 15;
                                                           Score 2181.5; DB 15; Length 449;
Pred. No. 2.4e-142;
8; Mismatches 20; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                              Gaps
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	Qy 435 SKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG 473 	
PVLDSDGSFFLY 434	QY 375 VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY	
ISKAKGQPREPQ 374 · ISKAKGQPREPQ 350	Qy 315 KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ 	
NWYVDGVEVHNA 314	QY 255 PCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA 	
EPKSCDKTHTCP 254	QY 195 HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCP 	
VSWNSGALTSGV 194 	QY 135 GQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGV 	
NGGFDYW 134 	Qy 80 ADSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFDYW	

Search completed: September 12, 2003, 13:06:06 Job time: 32.7966 secs

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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                         score greater than or equal and is derived by analysis of
                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                          1129
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1108.5
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        100.0
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                                                                                                                                                                                                                                                                                                                                             is the number of results predicted by chance to have a ster than or equal to the score of the result being printed,
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Maximum Match 100%
Listing first 45 summaries
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1: /SIDS1/gcgdata/g
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SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa199.DAT:*

SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa200.DAT:*

SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa200.DAT:*

SIDS1/gcgdata/geneseq/geneseqp-emb1/Aa200.DAT:*

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/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1983.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:*
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                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                           analysis of the total score distribution.
                                                                                                                                                                                                                          DB
           ij
    AAO14066
ABU08018
AAY92239
AAG71272
ABG63490
AAY93702
AAY93729
ABP71366
AAY93708
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Light chain protei Human monoclonal r Human bone marrow-human gene 2-encod Human albumin fusi The kappa chain of Anti-OPGL-1 antibo The kappa chain of
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ALIGNMENTS

RESULT 1 AAO14066 ID CARREST CONTRACTOR HRIG; human rabies-immune globulin; monoclonal; virucide; heavy chain; human monoclonal rabies virus neutralising antibcdy; immunoglobulin; light chain; central nervous system; CNS; prophylactic therapy; clone JA. (UYJE-) UNIV JEFFERSON THOMAS 16-MAY-2000; 2000US-204518P. 04-MAY-2001; 2001WO-US14468. 22-NOV-2001 WO200188132-A2 Homo sapiens. Light chain protein of the monoclonal antibody from clone JA 07-MAY-2002 AAO14066; AA014066 standard; Protein; (first entry) 234 A

WPI; 2002-062381/08 N-PSDB; AAK98702.

Hooper DC,

Dietzschold

В;

Novel isolated human monoclonal rabies virus neutralising antibody

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                                                                                 Hooper DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody; constant region; monoclonal antibody 57; Mab 57; variable region; Rables; neurological disease; infection central nervous system; rables virus; Lyssavirus; Rhabdoviridae; pathogen; vaccine; virucide; light chain.
     N-PSDB;
                                                                                                                                      (UYJE-) UNIV JEFFERSON THOMAS
                                                                                                                                                                                        21-AUG-2001;
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  2003-278566/27
DB; ABX12856.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention discloses a recombinant antibody comprising a constant cregion of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable cregion. Rables is an acute, neurological disease caused by infection of the central nervous system with the rables virus, a member of the Lysavirus genus of the family Rhabdoviridae. Also disclosed are methods for producing an isolated recombinant antibody by culturing a host cell, containing a recombinant expression vector comprising the nucleic acid molecule encoding the antibody, and isolating the recombinant antibody campitated and treating an individual the recombinant antibody. The recombinant antibody administering to the individual the recombinant antibody. The recombinant campistering to the individual the recombinant antibody. The recombinant capsed to a pathogen, e.g. rables infection. They are also useful for the gualitative and quantitative determination of the rables virus. The sequences presented are the antibody protein fragments, the nucleic acids encoding them or the PCR primers used to construct the recombinant
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Best Local :
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                                                                                   Modified-site
                                                                                                                                                                                                    antiparasitic
                                                                                                                                                                                                                                                                                        Human bone marrow-derived serum
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Best Local (
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 61
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GQAPRLLIYDASNRATGIPPRFSGSGSGTDFTLTISRLEPEDVALYYCQQYFTTPYTFGQ
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                                                                                                                                        Conservative
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                                                                                                                                 AAH31349-AAH31428 represent cDNAs corresponding to 26 human secreted protein genes, and AAG712319 represent the proteins they encode. AAG71320-AAG71301 represent the protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, arms anteriamnes diseases for rhenmatrid arthritis, inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; angiogenic disorder; kichey disorder; cardiovascular disorder; angiogenic disorder; kichey disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding a human secre:ed protein, usefu preventing, treating or ameliorating medical conditions such as rheumatoid arthritis, Alzheimer's disease and migrobial infections
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cell culture; chemotaxis; food additive;
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AIDS, autoimmune diseases (e.g., rheumatoid arthritis), infla allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, as skin disorders (e.g., psoriasis), sepsis, diabetes, atherosci

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Best Local S
Matches 218
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25-APR-2000;
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                                                    Rosen CA,
                                                                                                                                                                                                                                                                    12-APR-2001;
                                                                                                                                                                                                                                                                                                                        18-OCT-2001
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immunomodulator; anti-HIV; antidiabetic; haemostatic; nootropic;
neuroprotective; antiparkinsonian; antimicrobial; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albumin fusion protein; therapeutic protein; human albumin; human serum albumin; HSA; cancer; reproductive disorder; disorder; hmune disorder; endocrine disorder; haematopoietic disorder; neural disorder; connective disorder;
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                                                                                                         (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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2002-010886/01
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2000US-199384P.
2000US-256931P.
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No. 4.8e-64;
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Best Local S
Matches 218
Hanson DC,
Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                            Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft reject proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosing disorders such as cancer reproductive disorders, digestive disorders (e.g. Crohn's disease, ulcerative colitis), immune disorders (e.g. acquired immunodeficiency syndrome, AIDS), endocrine disorders (e.g. diabetes), haematopoietic disorders, neural disorders (e.g. Alzheimer's, Parkinson's, Creutzfeldt-Jacob disease, encephalomyelitis, meningitis, schizophrenia), and connective disorders (e.g. osteoporosis, arthritis). ABG63326-ABG65518 represent albumin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to albumin fusion proteins comprising a therapeutic protein X and human albumin (HA, also known as human serum albumin, HSA). The proteins are useful for treating a disease or disorder that may be modulated by therapeutic protein X. The albumin extends the shelf-life of protein X, and may increase its biological in vitro/in vivo activity. The protein is useful for treating and
                                                                           (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC
                                                                                                                                                                                                                23-DEC-1999;
                                                                                                                                                                                                                                                                  29-JUN-2000
                                                                                                                                                                                                                                                                                                                       WO200037504-A2
                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (e.g. osteoporosis, arthritis). A fusion proteins of the invention.
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                           Mueller
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Pred. No. 4
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                           Hanke
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                           JH,
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                           Gilman
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                           SC,
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                           Davis
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
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                     23-DEC-1998;
                                                                    23-DEC-1999;
                                                                                                                         29-JUN-2000
                                                                                                                                                                        WO200037504-A2
                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                               Homo
                                                                                                                                                                                                                                                                                                                                                                               proliferative
                                                                                                                                                                                                                                                                                                                                                                                                 Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93729;
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                     98US-0113647
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                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunoglobulin clone 4.1.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 3;
                                                                                                    Mus musculus
                                                                                                                         antiarthritic;
                                                                                                                                     Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
                                                                                                                                                            Anti-OPGL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                     Region
                                          Region
                                                                              Key
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                                                                                                                                                                                                         ABP71366;
                                                                                                                                                                                                                                ABP71366 standard;
                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        235 AA;
                                                                                                                                                          antibody kappa light chain.
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                                                                                                                         cytostatic;
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129..235
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                                                                          Location/Qualifiers
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91.5%;
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                                "variable region"
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                                                      signal peptide"
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Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system; hyperimmunity disorder; autoimmune disease; diabetes; graft reject proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to antibodies that interact with osteoprotegerin ligands (OPGL). The antibody is useful for detecting the level of OPGL in a biological sample. The antibody, or the pharmaceutical composition comprising the antibody, is also useful for treating osteopenic disorder, an inflammatory condition with attendant bone loss, an autoimmune condition with attendant bone loss in a pattent or rheumatoid arthritis in a pattent, in particular, the antibody or composition is useful for treating bone diseases, e.g. osteoporosis, bone loss from arthritis, paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
                                                                The
                                                                                               03-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes' syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                       QGTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
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                                                                                                                                                                                                                                                                                         QGTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNS
                                                           chain of immunoglobulin clone 6.1.1.
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                                                                                                                                                         Protein;
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Pred. No. 3.5e-6; Mismatches
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                 graft rejection;
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ha level of OPGL in
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Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;

disease; diabetes; graft rejection;

hyperimmunity disorder; autoimmune

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RESULT 10
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Matches 213
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The kappa chain of
                                  03-OCT-2000
                                                                                                     AAY93733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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DB; AAA46871.
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213; Conserv
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 immunoglobulin clone 6.1.1.
                                                                                                     Protein;
                                    entry)
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91.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    6;
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Pred. No. 5.8e-62;
6; Mismatches 15
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and light
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chain sequences,
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RESULT 1
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Best Local S
Matches 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
Peptide
 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                   AAR52951;
                                   AAR52951 standard;
                                                                                                                                                                                                                                                           Sequence
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)B; AAA46897.
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                                                                             ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 234
                                                                                                                GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                  GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWPWTFGQ
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(updated)
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                                   Protein;
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                                   234
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Pred. No. 5
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                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                ; DB 21;
5.8e-62;
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RESULT 12
AAY93704
ID AAY93
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AC AAY93
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03-OCT-2000 AAY93704;

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AAY93704

standard;

Protein;

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Query Match
Best Local
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(Updated on 25-MAR-2003 to correct PN field.)
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monoclonal anti-IgE peptide antibody - inhibits histamine release from mast cells by allergen stimulation, useful for preventing allergies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1992;
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Mast cells; Monoclonal antibody; allergy.
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DB; AAQ71872.
 181
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GTKVDLKGTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                              GTKVEFKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
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                                                                                                                                                                                                                                                                                                                  234 AA;
                                                                                                                                                                                                                                                    Conservative
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/label= light chain variable region
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Pred. No. 1.4e
10; Mismatches
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RESULT 13
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Matches 213
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                        AAY93731;
  03-OCT-2000
                                            AAY93731 standard; Protein;
                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
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Corvalan JR;
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entry;
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                                              233
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g and light
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Matches 213
                                                                                                                                                                                                                                                                              The present sequence represents a kappa chain of an antibody of the invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)-4. Antibodies of the invention are composed of a heavy chain variable region, comprising a modified contiguous sequence from a FRI-FR3 sequence encoded by a human VH3-33 family gene. The modifications are contained in CDR1, CDR2 and/or framework regions. The antibodies may be used to inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity disorders (e.g. autoimmune disease, diabetes and graft rejection) and proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be used to up-regulate immune system to up-regulate immunodeficient disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
Peptide
                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel antibodies capable of binding (CTLA)-4 containing specified heavy for treating, e.g. immune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune hyperimmunity disorder; autoimmune disease; diabetes; graff proliferative disorder; cancer; immunodeficient disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corvalan JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PFIZ ) PFIZER INC. (ABGE-) ABGENIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-DEC-1999;
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 180
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                                                                                                                                                                                                          al Similarity
213; Conser
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                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Fig 22k; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA46895
                                                                                                   ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
             ESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC
                                                   GTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQ
                                                                                                                                                      METPAQLLELLLULPDTTGEIVLTQSPGTLSLSPGERATLSCRTS-VSSSYLAWYQQKP
                                                                                                                                                                      MEAPAQLLFLLLLWLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                           233 AA;
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                                                                                                                                                                                                          Conservative
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1..20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunoglobulin clone 4.8.1
                                                                                                                                                                                                                     88.8%;
91.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mueller
                                                                                                                                                                                                       5;
                                                                                                                                                                                                       Score 1085.5; DB 21;
pred. No. 2.7e-61;
5; Mismatches 15; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytotoxic T-lymphocyte antigen and light chain sequences, use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hánke
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gilman
                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                  233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Davis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful
233
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RESULT 14 AAR12128

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Best Local (
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See also AAQ11879 and AAQ11880.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Peptide
                                                                                                                                                                                                                                                                                                                                                     Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of
                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                  Example 5; Fig 16; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IgG aberrant light chain with duplicated variable region
                                                                                                                                                                                                                                                                                                                                                                                        1991-163947/22.
DB; AAQ11878.
 61
                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lobulin G; light chain; variable region; duplication;
immunity; group B streptococci.
MEAPAQLLFLLLMLPDTTGEIVLTQSPATLSLSPGERATLACRASQTASRYLAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                          349
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          Harris
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(first entry)
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/note= "L'V 2"
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/note= "L'V 1"
131...243
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                                                                                                                                                                                                                                                                                                                                                                                                                            Raff HV;
                                                                                                     Score 1082.5; D
Pred. No. 6e-61;
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                                                                                            Mismatches
                                                                                                                  DB 12;
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ctiae. They are
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                                                                                     Oligomeric immunoglobulin(s) with high avidity for antigen(s) formed by duplicating esp. variable region of light chain of
                                                                                                                                                                              07-NOV-1989;
                                                                                                                                                                                             06-NOV-1990;
                                                                                                                                                                                                                16-MAY-1991
                                                                                                                                                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                                                                                                                            immunoglobulin passive immunit
                                                                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
01-AUG-1991
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                                                                                                                                                                                                                                                                                                                                                                                                       181 IgG aberrant light chain with duplicated variable region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13111
                                                            Example
                                                                                                                                                           (BRIM )
                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                          1991-163947/22
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                                                           5
                                                                                                                AAQ11878
                                                                                                                                                            BRISTOL-MYERS
                                                                                                                                                                                                                                                                                                                                                                           immunity; group B streptococci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVIKSFNRGEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FKRTVAAPSVFIFPPSDEOLKSGTASVVCLLNNFYPREAKYQWKVDNALQSGNSQESVTE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGTKVEIKHTTGEIVLTQSPATLSLSPGERATLSCRASQ FVGSYLAWYQQKPGQAPRPL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDSKDSTYSLSSTLTLSKADYEKHKYYACEYTHQGLSSPVfKSFNRGEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYQHRDNWPPGATFGGGTKVE
                                                          Fig
                                                                                                                                         Harris
                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                          16; 104pp;
                                                                                                                                                                             89US-0432700
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                                                                                                                                                                                                                                                                    /label= variable
/note= "L'V 2"
                                                                                                                                                                                                                                                                                       131..243
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18..130
                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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/note= "L'V l"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                            SQUIBB
                                                                                                                                                                                                                                                    constant region
                                                                                                                                          Raff HV;
                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414
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                                                                                                                                                                                                                                                                             region
                                                                                                                                                                                                                                                                                                                                                                                      region; duplication;
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This sequence is deduced from the cDNA clone 4B9·Vk15 and includes the amino acid sequence beyond the first stop cocon ("x" in the sequence represents a nonsense codon). The clone is incomplete, starting from the G of the ATG initiator codon, but the initial Met is given. Antibody molecules of the invention car include one or two aberrant light chains containing a duplicated variable region, to

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Search completed: September 12, 2003, 13:00:41 Job time: 41.9915 secs
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Best Local S
Matches 222
                                                                                                                                                                                                                                                                                                                                                   produce heavier antibodies. These heavier antibodies were found to have higher avidity than antibodies with just a single copy of the L'V region. The antibodies can be used to treat disease, e.g. infection by Streptococcus agalactiae. They are able to pass across the placenta. See also AAQ11879 and AAQ11880.
                                                                                                                                                                                                                                                                                                                                 Sequence
                                      126
                                                                                                                         181
                                                                                                                                             116
                                                                                                                                                                                     116
                                                                                241
                                                                                                                                                              121 GGGTKVEIKHTTGEIVLTQSPATLSLSPGERATLSCRASQSVGSYLAWYQQKPGQAPRPL 180
                                                                                                                                                                                                                                                                                        tch 88.5%; al Similarity 63.6%; 222; Conservative
                                                                                                                                                                                                         61
                                                                                                                                                                                                                            13
                                                                                                                                                                                                                                              GQAPRLLIYDTSNRATGIPARFSGSGSGTDFTLSISSLEPEDFAVYYCQQRFNWP----- 115
                                                                             IYDASNRATGIPARFSGSGSGTDFTLTISSLEPEDFAVYYCQHRDNWPPGATFGGGTKVE
                                                                                                                                    414 AA;
                                                                                                                                                                                                                                                                                       Score 1082.5; DB 12; Length 414; Pred. No. 7.1e-61; 3; Mismatches 9; Indels 115;
                                                                                                                                                                                                                                                                                        Indels 115; Gaps
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Run on:

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Minimum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                            seq length: 0
seq length: 2000000000
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Copyright (c) 1993 - 2003 Compus
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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                                US-08-157-101A-7
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US-09-027-449-71
US-09-121-952A-71
US-09-121-952A-71
US-09-121-952A-71
US-09-234-945A-2
US-09-680-148-2
US-09-680-148-2
US-09-680-148-2
US-09-109-207C-18
US-09-109-207C-18
US-09-282-846-2
US-09-282-846-2
US-09-282-846-2
US-09-887-352B-14
US-09-282-846-2
US-09-282-846-2
US-09-680-145-2
US-09-109-207C-14
US-09-109-207C-14
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748.902 Million cell updates/sec
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Sequence 71, Appl
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US-08-157-101A-7
                                                                                                                                                                 US-08-157-101A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08157101A Patent No. 5808032 GENERAL INFORMATION:
                                                             Query Match
Best Local (
                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KURIHARA, TATSUYA
MATSUKURA, SHIGEKAZU
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Result No.

45	44	3	42	41	40	39	38	37	36	35	34	ü	32	31	30	29	28
2037	2037	2044.5	2046	2046	2060	2062	2062	2086.5	2089	2090.5	2092	2092	2094.5	2100.5	2100.5	2104.5	2113
81.0	81.0	81.3	81.4	81.4	81.9	82.0	82.0	83.0	83.1	83.2	83.2	83.2	83.3	83.6	83.6	83.7	84.0
451	451	453	476	476	472	472	472	446	449	473	476	476	467	711	468	467	443
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US-09-466-635-3	US-09-247-352-3	US-09-301-593-18	US-09-526-098-4	US-08-487-550-4	US-09-301-593-30	US-09-301-593-43	US-08-793-450-8	US-08-397-411-7	US-08-458-516-13	US-09-049-672A-4	US-09-526-098-12	US-08-487-550-12	US-09-049-672A-8	US-09-485-737B-90	US-09-485-737B-67	US-08-704-744-81	PCT-US96-13152-4
ω ,	Sequence 3, Appli	18,	Sequence 4, Appli	Sequence 4, Appli	Sequence 30, Appl	Sequence 43, Appl	Sequence 8, Appli		Sequence 13, Appl	Sequence 4, Appli		Sequence 12, Appl	Sequence 8, Appli	Sequence 90, Appl	Sequence 67, Appl	Sequence 81, Appl	Sequence 4, Appli

ALIGNMENTS

Minimum

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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-861-3711
TELEPAX: 202-82-0944
TELEX: 6714627 CUCH
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                        ZIP: 2005
ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,101A
FILING DATE: 05-APR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: TITUS, MARLANA K
REGISTRATION NUMBER: 35843
REFERENCE/DOCKET NUMBER: 9437/204199
                                                                                               LENGTH: 459 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NISHIHARA, TATSURO
TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
TITLE OF INVENTION: PLASMIDS THEREFOR
Local Similarity nes 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 NEW CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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TSURUOKA, NOBUO
  Conservative
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                   88.4%; Score 2221.5;
89.9%; Pred. No. 2.1e
  19;
  Mismatches
                   .1e-172;
                                      DB 1;
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RESULT 2
US-09-027-449-71
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                                         ATTORNEY/AGENT INFORMATION:

NAME: LOVE, Richard B.

REGISTRATION NUMBER: 34,659

REFERENCE/DOCKET NUMBER: P108

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies.
NUMBER OF SEQUENCES: 72
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WINPALIA (Genentech)
CURRENT APPLICATION DATA:
APPLICATION MINISTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             PRIOR APPLICATION DATA: 22-Jan-1998
PRIOR APPLICATION NUMBER: 60/02
FILTURE TARREST TO PRICE TO PARTIE TO 
                                                                                                                                                                                                                                                            FILING DATE: 20-Feb-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/074,330
FILING DATE: 22-Jan-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1 DNA WAY
CITY: South San Francisco
STATE: Callfornia
COUNTRY: USA
ZIP: 94080
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TELEFAX:
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US-09-026-985-71
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Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Gonzalez, Tania R.
APPLICANT: Leong, Steven R.
APPLICANT: Leong, Steven R.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           STREET: 1 .... STREET: 1 CITY: South San Fra
                   ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 452 amino acids TYPE: Amino Acid TOPOLOGY: Linear
                                                                       APPLICATION NUMBER: FILING DATE: 20-Fe
                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                     ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416
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91.2%;
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Pred. No. 3.8e
9; Mismatches
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Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                  Sequence 71, Application US/09121952A Patent No. 6458355
GENERAL INFORMATION:
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                                                                                                             APPLICANT: Presta, Leonard G.
APPLICANT: Shahrokh, Zahra
APPLICANT: Shahrokh, Zahra
APPLICANT: Zapata, Gerardo A.
TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER (
NUMBER OF SEQUENCES: 72
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44
COMPUTER: IBM PC compatible
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LENGTH: 452 amino acids
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TELEPHONE: 650/225-5530
TELEFAX: 650/952-9881
                                  STREET: 1 DNA Way
CITY: South San F
STATE: California
COUNTRY: USA
ZIP: 94080
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REFERENCE/DOCKET NUMBER:
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                                                                                     1 DNA Way
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                                                                                                                                                                                              Leong, Steven
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Leonard G.
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91.2%;
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Pred. No. 3.8e
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3.8e-170;
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                                                                      RESULT 5
US-09-234-340A-71
Sequence 71, Application US/09234340A
Patent No. 6468532
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US-09-121-952A-71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 22-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/075
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 24-Jul-199
CLASSIFICATION: 514
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REFERENCE/DOCKET NUMBER: P1
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Amino Acid
LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 437
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                                                                      LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENIYKTTPPVLDSDGSFFLYSKL
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Koumenis, Iphigenia Leong, Steven R. Presta, Leonard G.

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INFORMATION FOR SEQ ID NO:
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TOPOLOGY: Line
-234-3/^-
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 452 amino acid
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FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09
FILING DATE: 24-Jul-1998
APPLICATION NUMBER: 60/07
FILING DATE: 22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P1085R4
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STATE: Californi
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                                                                                                                                                                                                                                                                                                                          ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGG--FDYWGQG 137
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                 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                                                                                                                                                                                                          NQKFKGRFTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGD----YRYNGDWFFDVWGQG
 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
                                                                                                                       APELLGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK
                                                                                                                                      APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK 317
                                                                                                                                                                                                                                                                                                                                                                        EVQLVQSGGGLVQPGGSLRLSCAASGYSFSSHYMHWVRQAPGKGLEWVGYIDPSNGETTY
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1 DNA Way
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91.2%;
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FI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
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US-08-487-550-8
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Anderson, I
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LENGTH: 478 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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COMPUTER: II
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STATE: VA
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                                                                                                       VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK 232
                                                                                                                                                                                                                                GKGLEWVSAI--SASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD 118
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                                                                                                                                                                                                                                                                          MGWSLILLFLVAVATRVQCEVQLVESGGGLVQPGGSLRVSCAVSGFTFSDHYMYWFRQAP
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VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN
                                            PSNTKVDKRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
                                                                                         VKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHK
                                                                                                                                                     --TSYISHCRGGVCYGGYFEFWGQGALVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCL
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                              PSNTKVDKKAEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVD
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86.7%;
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FO PHARMACEUTIAL COMPOSITIONS CONTAINING, IMMUNOSUPPRESANTS"
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Pred. No. 2.
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2.9e-169;
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Length 478; Indels

12;

Gaps

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                                                                                         Query Match
Best Local Similarity
Matches 418; Conserv
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                                                                                                                                                                                                                  TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 8:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
9-526-098-8
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
                                                                                                                                                                                                                                                       NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
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CITY: AL
STATE: V
COUNTRY:
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07-JUN-1995
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"MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
PHARMACEUTIAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESANTS"
                                                                                       86.8%; Score 2183; 1
86.7%; Pred. No. 2.90
Live 18; Mismatches
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                                                                                       ; DB 4;
2.9e-169;
hes 34;
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                                                                                                               Length 478;
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APPLICANT: BASEY, CAROL D.
APPLICANT: BLANK, GREG S.
APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1D2
CURRENT APPLICATION NUMBER: US/09/679,397
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
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                                                                                                                                                                                                      Query Match
Best Local 9
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                                                                                                                                                                                                                                                                                              LENGTH: 44
TYPE: PRT
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                                                                                       61 ADSVKGRFTISADTSKNTAYLQMNSLRAEDTAVYYCSR------WGGDGFYAMDYW
                                                                                                      80 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD\EVTMIVVLNGG-----FDYW
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                                     HTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKP;3NTKVDKRVEPKSCDKTHTCP
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                                                                                                                                                                                           Conservative
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Pred. No. 3.56
                                                                                                                                                                                          Mismatches
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APPLICANT: BASEY, CAROL D.
APPLICANT: BLANK, GREG S.
APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1D1
CURRENT APPLICATION NUMBER: US/09/680,148
CURRENT FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR APPLICATION NUMBER: US 09/304,465
PRIOR FILING DATE: 1999-05-03
NUMBER OF SEQ ID NOS: 2
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; OTHER INFORMATION:
; Patent No. 6417335
US-09-680-148-2
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US-09-680-148-2
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Best Local :
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TYPE: PRT
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                                        KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
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VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY
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                             KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQ
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ilarity 90.6%;
Conservative
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Pred. No. 3.5e
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US-08-466-151-8
; Sequence 8, Application
; Patent No. 6037453
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; OTHER INFORMATION:
; Patent No. 6489447
US-09-304-465A-2
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APPLICANT: BLANK, GREG S.
TITLE OF INVENTION: PROTEIN PURIFICATION
FILE REFERENCE: P1241R1
CURRENT APPLICATION NUMBER: US/09/304,465A
CURRENT FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/084,459
PRIOR FILING DATE: 1998-05-06
NUMBER OF SEQ ID NOS: 2
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GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Artificial sequence
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                                                                                                                                                                    VYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLY 434
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Pred. No. 3.5e-169;
8; Mismatches 20;
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Best Local
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185899
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APPLICATION NUMBER: C
FILING DATE: 06-Jun-)
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 453 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39,044
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APPLICATION NUMBER: 07/7
FILING DATE: 14-AUG-1991
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
TELEFAX: 650/952-9881
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CITY: South San F
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/1 FILING DATE: 26-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
TOPOLOGY: Linear
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   KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY
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                                 PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT
                                                   PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKT
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US-08-466-163B-8
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LENGTH: 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
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                                                                                             PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHI:DPEVKFNWYVDGVEVHNAKT
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                                 TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEHNYKTTPPVLDSDGSFFLYSK
                                                TLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEHNYKTTPPVLDSDGSFFLYSK
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Pred. No. 6.9e-169;
4; Mismatches 20;
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US-08-887-3528-18
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 451 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                            NAME: SVODOda, Craig G.
REGISTAGN NUMBER: 39,044
REFERENCE/DOCKET NUMBER: P1:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/887,352B
FILING DATE: 03-U1-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Improved Anti-IgE Antibodies
TITLE OF INVENTION: Improving Polypeptides
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WinPatin (Ge CURRENT APPLICATION DATA:
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                                LADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFDYWGQGT 138
PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
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Pred. No. 1.7e-168;
13; Mismatches 23;
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          RESULT 15
US-09-282-505-2
; Sequence 2, Application U
; Patent No. 6194551
; GENERAL INFORMATION:
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LENGTH: 451
TYPE: PRT
ORGANISM: Artificial
FEATURE:
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US-09-109-207C-18
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Best Local Similarity
  APPLICANT:
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; OTHER INFORMATION: Heavy chain sequence US-09-109-207C-18
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                                                                                             PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT 438
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VDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                        PPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLT
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90.8%;
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Pred. No. 1.7e-168;
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: LENGTH: 451
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: NAME/KEY: Artificial Sequence
: LOCATION: 1-451
: OTHER INFORMATION: Sequence is completely synthesized
: Patent No. 6194551
US-09-282-505-2
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Search completed: September 12, Job time: 28.7797 secs
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FILE REFERENCE: 91266R1
CURRENT APPLICATION NUMBER: US/09/282,505A
CURRENT FILING DATE: 1999-03-31
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 451
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Copyright (c) 1993 - 2003 Compugen
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26.7	26.8	27.0	27.1	27.3	27.5	27.5	27.5	27.7		27.9		29.7	29.7	29.7	30.0	30.0	30.0	30.1	30.1	30.8	32.3	32.7	33.7	34.5	35.7	36.1	36.9	37.0
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Q91WR1	Q8VCX4	Q8K0F2	Q96KX8	Q8K0Z4	Q8K172	Q96DK0	Q91X92	Q91WT1	Q99LA6	Q8WY24	Q9BRV0	Q96AA6	Q8WUX4	Q96EY0	д9вдв8	Q96GA6	Q921K1	010860	Q8VCX7	Q8WU38	Q8VEA0	Q91xE1	Q91Z07	Q91WP5	Q99KA4	Q8NCL6	Q8N5K4	Q96K68
Q91wr1 mus musculu	Q8vcx4 mus musculu	Q8k0f2 mus musculu	homo	Q8k0z4 mus musculu	Q8k172 mus musculu	homo	mus	Q91wt1 mus musculu	6 mus	Q8wy24 homo sapien	Q9brv0 homo sapien	homo	homo	homo		homo	l mus	homo		homo	mus	Q91xe1 mus musculu	Q91z07 mus musculu	Bum	4 mus	homo	Q8n5k4 homo sapien	Q96k68 homo sapien

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QBTC77;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted [FEB-2002) to the EMBL/GenBank/DDBJ databases EMBL; BC024289; AAH24289.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_WHC.
Pfam; PF00047; ig; 4.
SMART; SM00406; IG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
Hypothetical protein.
SEQUENCE 471 AA; 51791 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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61 GKGLEWVSSMSSSSSYIYYADSVKGRFTISRDNAKNSLYL\MNSLRAEDTAVYYCARDLR 120
                                                61 GKGLEWVSAISASGHSTYLADSVKGRPTISRDNSKNTLYL/)MNSLRAEDTAVYYCAKD-R 119
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51791 MW;
                                                                                                                                                                                                                                                                                                                                   92.5%; Score 2325.5; DB 4; Length 471;
92.2%; Pred. No. 2.2e-183;
tive 19; Mismatches 13; Indels 5;
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Q8N4Y9;
Q1-CCT-2002 (TrEMBLrel. 22, Crea
Q1-CCT-2002 (TrEMBLrel. 23, Last
Q1-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical protein
Homo sapiens (Human),
Eukaryota; Metazoa; Chordata; C1
Mammalia; Eutheria; Primates; Ct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (JUN-2002) to the EMB Submitted (JUN-2002) to June (June Submitted (
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TISSUE=Primary B-C
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein. SEQUENCE 521 AA;
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                                                                                                                                                                                                                                                                                                                                                                      404;
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                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                      GKGLEWVSAISASGH--STYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKD
                                                  EPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57156 MW;
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Last sequence
Last anno
                                                                                                                                                                                                                                                                                                                                                                 Score 2105.5; DB 4
Pred. No. 3.6e-165;
6; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2AC7D22E72D6CAA2 CRC64;
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annotation
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Best Local S
Matches 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (MAR-2002) to the EMBL, EMBL; BC025985; AAH25985.1; -. Interpro; IPR000923; BlueCu_1. Interpro; IPR000923; BlueCu_1. Interpro; IPR003006; Ig_MHC. Interpro; IPR003006; Ig_MHC. Interpro; IPR003506; Ig_v. Pfam; PF00047; Ig; 4. SMART; SM00406; IGv; 1. PR0SITE; PS00196; COPPER_BLUE; 1 PR0SITE; PS00196; COPPER_BLUE; 1 PR0SITE; PS00290; IG_MHC; 3. Hypothetical protein. SEQUENCE 473 AA; 51986 MW; E:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTC63 PRELIMINARY; PRT;
OSTC63 PRELIMINARY;
OSTC63 PRELIMINARY;
O1-JUN-2002 (TrEMBLrel. 21, Last seq
O1-MAN-2003 (TrEMBLrel. 23, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
     184
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                                                                                                                                                                                                                                                                                                                                                                                                                368;
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MIVVLNGGED-YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
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Primates;
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77.88;
                                                                                                                                                                                                                                                                                                                                                                                                              31;
                                                                                                                                                                                                                                                                                                                                                                                                           Score 1882; D
Pred. No. 8.7e
31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E29920B09BA369F5 CRC64;
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annotation
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3.7e-147;
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Best Local S
Matches 307
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Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ dat
EMBL; BCO24405; AAH24405.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003106; Ig_wHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
R PROSITE; PS050835; IG_LIKE; 4.
R PROSITE; PS050835; IG_LIKE; 4.
R PROSITE; PS050835; IG_MHC; 1.
W Hypothetical protein.
SEQUENCE 469 AA; 51976 MW; 534793F155D05457 (
                                                                                                                                                                                                                                                                                                                                                                                                                                    Q8R3V9 PRELIMINARY; PRT; 469 AA.
Q8R3V9;
Q8R3V9;
r 01-JUN-2002 (TrEMBLrel. 21, Created)
r 01-JUN-2002 (TrEMBLrel. 22, Last sequence update)
r 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
r pypothetical 52.0 kDa protein.
Hypothetical 52.0 kDa protein.
Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Eumammalia; Eutheria; Rodentia; Sciurognathi; Muridae; M
                                                                                                                                                                                                                                                           Local Similarity
                    297
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                                                                                                                                                              TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
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                                      PPVLDSDGSFFLYSRLTVDKSRWQEGNVFSCSVMHEALHNHYTQKSLSLSLGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
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 DPEVQFSWFVDDVEVHTAQTKPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFP
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                66.1%; Score 1660.5; DB 11; Length 64.2%; Pred. No. 1.6e-128; Elve 72; Mismatches 86; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                          534793F155D05457 CRC64;
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; Murinae; Mus
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Best Local S
Matches 309
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Spleen;
Jikuya H., Takano J., Kikuno R., Nagase T., Ohara.
"The nucleotide sequence of a long cDNA clone iso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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IPR003597;
IPR003006;
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                                                                  KGFYPSDIAVEMESNGQPENNYKTTPPVLDSDGSFFLYSKIJVDKSRWQQGNVFSCSVMH
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™+heria; Primates; (
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Ig_MHC.
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Last annotation updat
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Catarrhini; Hominidae;
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RESULT

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O91205;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence upda:
O1-MAR-2003 (TrEMBLrel. 23, Last annotation up)
Hypothetical 51.9 kDa protein.
01044919.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Verteb.
Musmuslia; Eutheria; Rodentia; Sciurognathi; Mu
NCB1_TaxID=10090;
[1]
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 3
SMART; SM00406; IG; 1.
PROSITE; PS00190; CYTOCHROME_C; 1.
PROSITE; PS00190; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ
EMBL; BC010327; AAH10327.1; -
MGD; MGI:2144967; AU044919.
MGD; MGI:2144967; AU044919.
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Pred. No. 1.7e
70; Mismatches
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RESULT

Q9D8L4

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RESULT 8
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OPRIA4;
OPRIA4;
O1-MAY-2000 (TrEMBLrel. 13, L.
O1-MAY-2003 (TrEMBLrel. 23, L.
O1-MAR-2003 (TrEMBLrel. 23, L.
Gammal heavy chain of Mab7 (FIGH-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
NON_TER
SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        single chain antibody (scFV Submitted (MAY-1999) to the EMBL; AF152372; AAD40243.1; HSSP; P01842; 7FAB. MGD; MGI:96446; Igh-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.; "Cloning of cDNAs encoding for anti-white pine blister rust antibody (mab 7, its light and heavy chains) and construction single chain antibody (scFV).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
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                                                                                                                                                                                                                                                                                                       PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYT
|||||:||:|| || || :||:||||||||:||:||:||
PREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGRPKAPQVYT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDREVTMIVVLNGGFD-YWGQGTR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS00290; IG_MHC;
                                                                                                                  NVQKSNWEAGNTFTCSVLHEGLHNHHTEKNLSHSPGK
                                                                                                                                                                                                                                     LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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437 /
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63.0%;
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Last sequence up
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RX MEDLINE-C27BL/G; TISSUE-Pancreas;
RX MEDLINE-C2108566; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schrimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boiftelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Asaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local S
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Mus musculus (Mouse).
Rukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
EMBL; AK007918; BAB25349.1; -.
HSSP; P01842; 7FAB.
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01-JUN-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
1810060009R1K protein.
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PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00250; IG_MRC; 1.
SEQUENCE 473 AA; 51699 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig; 4. SMART; SM00406; IGv;
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277; Conserv
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; IPR007110; I:
; IPR003006; I:
VVDVSEDDPDVQISWFVNNVEVHTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCK
                  VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK
                                                          TKVDKKIEPRVPITQNPCPPLKECPPCAAPDLLGGPSVFIFPPKIKDVLMISLSPMVTCV
                                                                          TKVDKRVEPK-----SCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCV
                                                                                                                                     YFPEPVTVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
                                                                                                                                                                                                                                                           GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDRE
                                                                                                                                                                                                                                                                                                                   MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
                                                                                                                                                                                                            VTMIVVLNGGFD----YWGQGTRVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKD
                                                                                                                                                                                                                                          GQGLEWIGKIGPGSGSTYYNEKFKGKATLTADKSSSTAYMQLSSLTSEDSAVYFCAR---
                                                                                                                       YFPEPVTLTWNSGSLSSGVHTFPALLQ-SGLYTLSSSVTVTSNTWPSQTITCNVAHPASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                                                                                SGYDYDWFAYWGQGTLVTVSAAKTTAPSVYPLAPVCGGTTGSSVTLGCLVKG
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57.1%;
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17,
23,
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Pred. No. 3.2e-116;
"Hematches 100;
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Last sequence update)
Last annotation updat
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Query Match
Best Local S
Matches 274
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InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 463 AA; 51007 MW; 1
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Q99LC4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (FEB-2001) to the EMBL/GenBank/DDBJ EMBL; BC003435; AAH03435.1; - HSSP; P01842; 7FAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Similar to RIKEN cDNA 1810060009 gene.
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274;
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74; Conservative
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                                                                 KIVPRDCG---
                                                                                                                                 VTVTWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVPSSTVPSETVTCNVAHPASSTKVDK
                                                                                                                                                                                                   VTVSWNSGALTSGVHTEPAVLQSSGLYSLSSVVTVPSSSIGTQTYICNVNHKPSNTKVDK
                                                                                                                                                                                                                                                     YSYDL----FAYWGQGTLVTVSAAKTTPPSVYPLAPGS! AQTNSMVTLGCLVKGYFPEP
                                                                                                                                                                                                                                                                     VTMIVVLNGGFDYWGQGTRVTVSSASTKGPSVFPLAPSSISTSGGTAALGCLVKDYFPEP
                                                                                                                                                                                                                                                                                                                     GQGLEWVGEIYPGSGNTYYSEKFKGKATLTTDKSSSTAYHLLSSLTSEDSAVYFCARSSY
                                                                                                                                                                                                                                                                                                                                      GKGLEWVSAISASGHSTYLADSVKGRFTISRDNSKNTLYIQMNSLRAEDTAVYYCAKDRE
                                                                                                                                                                                                                                                                                                                                                                                  MEFGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
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                                                   EVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMH(;DWLNGKEFKCRVNSAAFPAP
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                                                                                                                   -CKPCICTVPEV---SSVFIFPPKPKDVI/TITLTPKVTCVVVDISKDDP
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57.6%; Pred. No. 6.6e-1
tive 85; Mismatches 1
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RESULT
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003096; Ig_v.
Pfam; PF00047; Ig; 3.
SMARP; SW00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
SEQUENCE 468 AA; 51661 MW; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Similar to RIKEN CDNA 1810060009 gene.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammaalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (FEB-2001)
EMBL; BC003878; AAH03
HSSP; P01842; 7FAB.
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||: ||:|: | | ||:|| :|| ||:|| |::|| ||:|| :|
| SWVIFFLMAVVIGVNSEVQLQQSGAELVRPGASVKLSCTASGFNIKDSLMHWVKQRPEQG
                                                                                                                                                            TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTT
                                                                                                                                                                                                                                  FNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK
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                                                                                                                                          TISKPKGSVRAPQVYVLPPPEEEMTKKQVTLTCMVTDFMPEDIYVEWTNNGKTELNYKNT
                                                                                                                                                                                                                ISWFVNNVEVLTAQTQTHREDYNSTLRVVSALPIQHQDWMSGKEFKCKVNNKALPAPIER
                                                                                                                                                                                                                                                                                   PKSCDKTHTCPP--CPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVK
                                                                                                                                                                                                                                                                                                                                                       TWNSGSLSSGVHTFPAVLQSD-LYTLSSSVTVTSSTWPSQSITCNVAHPASSTKVDKKIE
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Pred. No. 4e-113;
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   RESULT 12
Q8R3H6
ID Q8R3H
AC Q8R3H
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DT 01-JU
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Best Local S
Matches 274
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 3.
SMART; SM00406; IGv; 1.
PR0SITE; PS50835; IG_LIKE; 4.
PR0SITE; PS00290; IG_MHC; 1.
SEQUENCE 473 AA; 52449 MW;
Q8R3H6;
Q8R3H6;
Q1-JUN-2002
Q1-JUN-2002
Q1-MAR-2003
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099L25 O1-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence up
01-MAR-2003 (TrEMBLrel. 23, Last annotation
Similar to RIKEN CDNA 1810060009 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-2001) to the EMBL; BC003888; AAH03888.1; HSSP; P01842; 7FAB.
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                                                                                                                                                                            SLSPGK
                                                                                                                                                                                                                               MEEGLSWLFLVAILKGVQCEVQLLESGGGLVQPGGSLRLSCAASGFTFSNYAMSWVRQAP
||:::||::::||:||:||
|MEWSWVFLFFLSVTTGVHSQVQLQQSDAELVKPGASVKISCKVSGYTFTDHTIHWVKQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                      -----GGSIYYGYGLYYFDYWGQGTTITVSSAKTTAPSVYPLAPVCGDTTGSSVTLG
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 (TrEMBLrel.)
(TrEMBLrel.)
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                                                                       PRELIMINARY;
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   21,
21,
23,
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Last
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                                   Created)
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Pred. No. 7.5e
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Best Local S
Matches 268
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SMART; SM00406; IGv 1.

PROSITE; PS00190; CYTOCHROME_C; 1.

PROSITE; PS0035; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 1.
                   Q95M34 PRELIMINARY;
Q95M34;
01-DEC-2001 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Immunogobulin gamma 1 hee
Equus
            IGHC1
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                                                                                                                                                                         TEENYKDTAPVLDSDGSYFIYSKLDIKTSKWEKTDSFSCNVRHEGLKNYYLKKTISRSPG
                                                                                                                                                                                    PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                                                                                                                                                                                                   DLPSPIERTISKIKGLVRAPQVYILPPPAEQLSRKDVSLTCLVVGFNPGDISVEWTSNGH
                                                                                                                                                                                                                              ALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQ
                                                                                                                                                                                                                                                             SHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNK
                                                                                                                                                                                                                                                                                                                                                                                            ----YGDYFDDWGQGATVTVSSAKTTPPSVYPLAPGCGDTTGSSVTLGCLVKGYFPES
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                                                                            PRELIMINARY;
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rel. 19,
rel. 23,
1 heavy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%; Score 1414; 55.7%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79;
                    Created)
Last sequence update)
Last annotation update)
chain constant region (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ore 1414; DB 11;
ed. No. 3.6e-108;
Mismatches 120;
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Best Local
                                                                                                                                                                                                              Q96FQ8 PRELIMINARY; PRT; 701 AA.
Q96FQ8;
01-DEC-2001 (TrEMBLrel. 19, Created)
10-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
10-MAR-2003 (TrEMBLrel. 23, Last annotation update)
11-DEC-2001 (TrEMBLrel. 23, Last annotation update)
11-DEC-2001 (TrEMBLrel. 23, Last annotation update)
12-DEC-2001 (TrEMBLrel. 19, Last annotation update)
13-DEC-2001 (TrEMBLrel. 19, Last sequence update)
14-DEC-2001 (TrEMBLrel. 19, Last sequence update)
15-DEC-2001 (TrEMBLrel. 19, Last sequence update)
16-DEC-2001 (TrEMBLrel. 19, Created)
16-DEC-2001 (TrEMBLrel. 19, Created)
16-DEC-2001 (TrEMBLrel. 19, Created)
17-DEC-2001 (TrEMBLrel. 19, Created)
18-DEC-2001 (TrEMBLrel. 19, Created)
19-DEC-2001 (TrEMBLrel. 19, Last sequence update)
1
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SMART; SM00407; IGC1; 2.

PROSITE; PS50835; IG_LIKE; 3

PROSITE; PS00290; IG_MHC; 2.

NON_TER 1 1
MEDIANE-21477448; PubMed=11595054,
MEDIANE-21477448; PubMed=11595054,
Hu Z., Garen A.;
"Targeting tissue factor on tumor vascular endothelial cells
"Targeting tissue factor on tumor vascular endothelial cells
"Targeting tissue factor on tumor vascular endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
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EMBL; AJ300675; CAC44624.1; -.
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Leibold W., Radbruch A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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Mammalia; Eutheria;
                                                                                                                                                         SEQUENCE FROM N.A.
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Pred. No. 5.8e
44; Mismatches
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Best Local S
Matches 230
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R InterPro; IPRO00152; Asx_hydroxy1.
R InterPro; IPRO00134; EGF_Ca.
R InterPro; IPRO00188; EGF_Ca.
R InterPro; IPRO00208; EGF_Like.
R InterPro; IPRO002383; GLA_blood.
R InterPro; IPRO03096; Ig_AL_blood.
R InterPro; IPRO03096; Ig_MRC.
R InterPro; IPRO03096; Ig_MRC.
R InterPro; IPRO03096; Ig_MRC.
R InterPro; IPRO03094; VitK_dep_GLA.
R InterPro; IPRO00294; VitK_dep_GLA.
R Pfam; PF00008; EGF; 2.
R Pfam; PF000047; Ig; 2.
R Pfam; PF000094; gla; 1.
R Pfam; PF00009; EGF; 2.
R PFAMT; PR000010; EGF=DLOOD.
R PRINTS; PR000010; EGF=DLOOD.
R PRINTS; PR000010; EGF=Ca; 1.
R PRINTS; PR000019; GLAB_LOOD.
R PRINTS; PR000019; GLAB_LOOD.
R PRINTS; PR000019; GLAB_LOOD.
R PRINTS; PR000010; GLAB_LOOD.
R PRINTS; PR000010; GLAB_LOOD.
R PRINTS; PR000010; GLAB_LOOD.
R PRINTS; PR000010; EGF=Ca; 1.
R PROSITE; PS00010; ASX_HYDROXYL; 1.
R PROSITE; PS000010; ASX_HYDROXYL; 1.
R PROSITE; PS000011; GLU_CARBOXYLATION; 1.
R PROSITE; PS000013; GLU_CARBOXYLATION; 1.
R PROSITE; PS000013; TRYPSIN_DOM; 1.
R PROSITE; PS000134; TRYPSIN_BER; 1.
R PROSITE; PS000134; TRYPSIN_SER; 1.
EGF=11ke domain; Hydrolase; Protease; Serine protes
Q96BB9 PRELIMINARY;
Q96BB9;
01-DEC-2001 (TrEMBLrel. 19, L.
01-DEC-2001 (TrEMBLrel. 23, L.
H)pothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBT_TaxID=9606;
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-!- SIMILARITY: BE
EMBL; AF272774; AA
HSSP; P00761; 1AN1
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230; Conserv
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nilarity 99.1%;
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                                  Primates;
                                                                 Chordata;
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TO PER
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Pred. No. 5.7e
2; Mismatches
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                                                                                                                                                  Created)'
Last sequence update)
Last annotation update)
                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                               PRT;
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Query Match
Best Local S
Matches 240
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EMBL; BC015760; AAH15760.1; .
InterPro; IPR0031016; Ig-1ike.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 5.
SMART; SM00406; IGv. 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
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SEQUENCE FROM N
TISSUE=B-céll;
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al Similarity 40.5%;
240; Conservative 73
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MPEPQAPGRYFAHSILTVSEEEWNTGETYTCVVAHEALPNRVTERTVDKSTGK
                         VLD--SDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK
                                                                                                                              GVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKGLEWVSAISGSGGSTYYADSVKGRFTISRDNSRDTLYLQMNSLRAEDTAVYYCAKDPR
                                                                                                                 NGEAVKTHTNISESHPNATFSAVGEASICEDDWNSGERFTCTVTHTDLPSPLKQTISRPK
                                                                                                                                                                         TFQQNASSMCVPDQDTAIRVFAIPPS-FASIFLTKSTKLTCLVTDLTTYD-SVTISWTRQ
                                                                                                                                                                                                                                 QVSWLREGKQVGSGVTTDQVQAEAKESGPTTYKVTSTLTIKESDWLSQSMFTCRVDHRGL
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                                                                                                                                                                                                                                                            -PCPAPELLGGPS-----
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Pred. No. 6.1e
73; Mismatches
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Search completed: September 12, 2003, 13:03:27 Job time: 85.3475 secs

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Minimum
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re greater than or equal to the score of the result being printed
is derived by analysis of the total score distribution.
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Gapop 10.0 ,
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MEDLINE=71064027; PubMed=4923144;
Gall W.E., Edelman G.M.;
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Ponsting1 H., Hilschmann N.;
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Rutishauser U., Cunningham
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Cunningham B.A., Rutishauser U., Gall W.E.,
Waxdal M.J., Edelman G.M.;
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and its complex with fragment B of protein A from Staphylococcus

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E Biochemistry 20:2361-2370(1981)

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MEDLINE=95255298; PubMed=7737190;
Stoppini M., Bellotti V., Negri A.,
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"The primary structure of a human IgG2 heavy
evolutionary, and functional implications.";
J. Immunol. 125:1048-1054(1980).
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"Linkage and sequence homology of two human immunoglobulin heavy chain constant region genes.";
heavy chain constant region genes.";
Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
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MEDLINE-80114419; PubMed-118920;
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Mol. Immunol. 16:923-925(1979).
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"Characterization of the immunoglobulins.";
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J. Biochem. 57:758-767(1979).
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"Structural studies of immunoglobulin
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"Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.; "Heavy chain genes of rabbit 190: isolation of a cDNA encodin heavy chain and identification of two genomic C gamma genes." Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
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P01862;
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                     Pfam; PF00047; 19; 2.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                      Oliveira B., Lamm M.E.; "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
                                                                                                                                                                                                                                                                                                                                          MEDLINE=71058474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the CH2 homology antibodies.";
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"Structure of heavy chain from strain 13 guinea immunoglobulin-G(2). II. Amino acid sequence of and hinge region cyanogen bromide fragments.";
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Mammalia; Eutheria;
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Trischmann T.M., Cebra
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chemistry 10:9-17(1971).
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Cebra J.J.;
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REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN WEDLINE-77021516; PubMed-823945; Wolfenstein-Todel C., Frangione B., Prelli F., Fr "The amino acid sequence of 'heavy chain disease' Structure of the Fc fragment of immunoglobulin G3
                                                                                                                                                                                                                                               SEQUENCE (DISEASE PROTEIN WIS).

MEDLIND-8102L548; PubMed-6774747;

Frangione B., Rosenwasser E., Prelli F., Franklin I

"Primary structure of human gamma 3 immunoglobulin
gamma 3 heavy-chain disease protein Wis.";

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     GO; GO:0005624; C:membrane fraction; NAS.
GO; GO:0003823; F:antigen binding activit
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003597; Ig_cl.
InterPro; IPR003065; Ig_MHC.
Pfam; PF00407; Ig; 2.
SMART; SM00407; IGcl; 1.
MOD_RES
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 2
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM;
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HSSP; P01857; 1FC1.
Genew; HGNC:5527; IGHG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem.
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MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS I MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAREF 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: DISEASE PROTEIN WIS
AND ALL OF THE CH1 REGION.
MISCELLANEOUS: DISEASE PROTEIN ZUC
OF THE CH1 REGION, AND PART OF THE
GAMMA-3 HEAVY CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Excupean Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
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MISCELLANEOUS: THE HINGE REGION IN GAMM TIMES AS LONG AS IN OTHER GAMMA CHAINS IDENTICAL 15-RESIDUE SEGMENTS PRECEDED COMMENT.
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                                                                                                                                                                                  Pfam; PF00047; 19; 3.
SMART; SM00407; IGC1; 2.
PROSITE; PS50835; IG_LIKE; 3.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                              Gene 74:473-482(1988).
PIR; PS0017; PS0017.
HSSP; P01842; 7FAB.
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InterPro; IPR003597;
InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ig gamma-1 chain C region Rattus norvegicus (Rat).
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Rodentia;
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T -> A (IN OMM).
/FTId=VAR_003893.
S -> N (IN OMM).
/FTId=VAR_003894.
MISSING (IN ZUC).
/FTId=VAR_003895.
F -> Y (IN OMM).
/FTId=VAR_003896.
INTERCHAIN
                                                                 CH1.
HINGE.
CH2.
CH3.
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F -> Y (IN OMM).
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/FTId=VAR_003890.
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ID GC3_M
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EMBL; J00451; -; NOT P
PIR; B02156; G3MSC.
HSSP; P01857; IFC1.
InterPro; IPR007110; I
InterPro; IPR003597; I
InterPro; IPR003006; I
Pfam; PF00047; ig; 3
SMART; SM00407; IGC1;
                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GC3_MOUSE STANDARD;
p22436;
01-AUG-1991 (Rel. 19, Creat
01-AUG-1991 (Rel. 19, Last
16-OCT-2001 (Rel. 40, Last
                                                                                                                                                                                                                                                                                                                                                           MEDIINE-85027161; PubMed-6092053; Wels J.A., Word C.J., Rimm D., Der-Tucker P.W., Blattner F.R.; "Structural analysis of the murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebratu; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
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:||||| |:|||:|| ||||:|:||| |||| ||||
EKWQQGNTFTCSVLHEGLHNHHTEKSLSHSPGK 326
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Last sequence update)
Last annotation updat
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Pred. No. 3
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Best Local S
Matches 215
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SEQUENCE FROM N.A.
MEDLINE-80045036; PubMed-115593;
MEDLINE-80045036; PubMed-115593;
Obata M., Yamawaki-Kataoka Y., Kataoka
                                                                                                                                                                                                                                                                     GC1_MOUSE STANDARD; PRT; 3: P01868; P1 1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation if gamma-1 chain C region secreted for
                                                           Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., (Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.; "Immunoglobulin gamma I heavy chain gene: structural gene cloned in a bacterial plasmid."; Gene 9:87-97(1980).
MEDLINE-80012837; PubMed-1137
Rogers J., Clarke P., Salser
"Sequence analysis of cloned
heavy chain.";
                                                                                                                 MEDLINE-80202559; PubMed-6769752;
                                                                                                                         SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
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DOMAIN
DOMAIN
                                                                                                                                                          "Cloning and complete nucleotide gamma 1 chain gene.";
                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                  NCBI_TaxID=10090;
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                                           EQUENCE
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                            OF 70-322 FROM N.A. (MYELOMA 80012837; Pubmed-113776;
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329
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36228 MW;
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65.0%;
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Pred. No. 7e-7
14; Mismatches
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Sciurognathi;
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chi; Muridae; Murinae; Mus
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        part
                                                                                           Kataoka T., Shimizu A.,
P., Honjo T.;
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EMBL; V00793; CAA24173.1; -.
EMBL; V00793; CAA24174.1; -.
EMBL; V00793; CAA24175.1; -.
EMBL; V00795; CAA24176.1; -.
PIR; A02159; GIMS.
PDB; 11GC; 03-JUN-95.
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                                                                                      DISULFID
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                                                                                                                                                                                                                                                                                  InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
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InterPro; IPR007110; I
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GlycoSuiteDB; P01868; -.
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                                                                                                             CARBOHYD
                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                murine myeloma
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                                                                                                                                                                                                                                            Alternative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Evolution of immunoglobulin subclasses. murine myeloma gammal chain.";
J. Biol. Chem. 253:6068-6075(1978).
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[4]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note-May be the major isoform;
Name-Membrane-bound;
IsoId-P01869-1; Sequence-External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event-Alternative splicing; Named iso
Name-Secreted;
IsoId-P01868-1; Sequence-Displayed;
             Similarity
  Conservative
                                                                                                                                                                                                                                           splicing;
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                                           35704
            45.5%;
62.3%;
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                                             MW;
  55;
                                                                                                                                INTERCHAIN
INTERCHAIN
INTERCHAIN
INTERCHAIN
Score 1145; DB 1;
Pred. No. 1.5e-71;
5; Mismatches 60
                                         REMOVED POST-TRANSLATIONALLY,
N -> D (IN REF. 3).
N -> D (IN REF. 3).
; A338812F3D1F2C93 CRC64;
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P20761;
01-FEB-1991 (Rel. 17, Crea
01-FEB-1991 (Rel. 17, Last
15-SEP-2003 (Rel. 42, Last
15-SEP-2003 (Rel. 42, Last
1g gamma-2B chain C region
Rattus norvegicus (Rat).
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DOMAIN
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NON_TER 1
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SMART; SM00407; IGc1; 2.

PROSITE; PS50835; IG_LIKE; 3

PROSITE; PS00290; IG_MHC; 1.
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                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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InterPro; IPR003597;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Evolution of the rat immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                               Local Similarity
mes 214; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                  e 74:473-482(1988).
SIMILARITY: Contains
                   145
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42, Last annotation
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IG-LIKE 2.
IG-LIKE 3.
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                                              Score 1144.5; DB 1; Pred. No. 1.7e-71; 5; Mismatches 68;
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Sciurognathi; Muridae;
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ID GC1M_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Honjo T., Obata M., Yamawaki-Kata Takahashi N., Mano Y.; Takahashi and complete nucleotide gamma 1 chain gene."; Cell 18:559-568(1979).
                                                                                                                                                                                                                                                    SEQUENCE OF 323-366 FROM N.A.
MEDLINE-82115295; PubMed-6799207;
Rogers J., Choi E., Souza L., Car
Eisenberg D., Wall R.;
                                                                                                                                                                                                                                                                                                                                          conserved transmembrane domain.";
                                                                                                                                                                                                                                                                                                                                                      Tyler B.M., Cowman A.F., Gerondakis S.D., "mRNA for surface immunoglobulin gamma ch conserved transmembrane sequence and a 28
                                                                                                                                                               SEQUENCE OF 1-44 FROM N.A MEDLINE=82222190; PubMed=
                                                                                                                                                                                                         "Gene segments encoding transmembrane immunoglobulin gamma chains."; Cell 26:19-27(1981).
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=82197626; PubMed=6804950;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 323-393 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=80045036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P01869;
                                                                                                     immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
                                                                                                                                              MEDLINE=82222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata
                                                                                                                                  "Nucleotide sequences of gene segments
                              Name=Secreted;
                                                                        Event=Alternative splicing;
                                                                                          ALTERNATIVE PRODUCTS:
                                                           Name=Membrane-bound
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 sequence=External;
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Sciurognathi; Muridue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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SMART; SM00407; IGc1; 2.
PROSITE; PS50835; IG_LIKE; 3
PROSITE; PS00290; IG_MHC; 1.
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; 1KCR; 11-MA
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                                                                                                                                                                                       GGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ
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RWQQGNVFSCSVMHEALHNHYTQKSLSLSPG
                                EQMAKDKVSLTCMITDFFPEDITVEWQWNGQPAENYKNTQPIMNTNGSYFVYSKLNVQKS
                                                         EEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKS
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IPR003597; Ig_cl.
IPR003006; Ig_MHC.
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24-JUL-02.

11-MAY-02.

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Pred. No. 4
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RESULT 12
GC3M_MOUSE
ID 3M_MOUSE
AC P03987;
DT 23-CCT-1986
DT 01-AUG-1991
DT 01-AUG-1991
DT 15-JUL-1999
DE IG gamma-3 os
SM um susculus
CC Eukaryota; PO CO MAMMMalia; EL
OX NCELITAXID--
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RT TUCKET P.W.
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RA WALL EMBO J 3:27
RN [2]
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EMBL; V01556; CAA24767.1; ALT_SEQ.
PIR; A02156; GAWA.
HSSP; P01857; 1FC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    segment.";
Nucleic Acids Res. 11:6775-6785(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wels J.A., Word C.J., Rimm D., Der-
Tucker P.W., Blattner F.R.;
"Structural analysis of the murine
EMBO J. 3:2041-2046(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-85027161; PubMed-6092053;
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Eukaryota; Metazoa; C
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Ig gamma-3 chain C region, membrane-bound for
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23-OCT-1986
                                                                                                                                                                                                                                                                   Transmembrane;
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                 146 STKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSSG
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l3; Conservative
TTTAPSVYPLVPGCSDTSGSSVTLGCLVKGYFPEPVTVKWNYGALSSGVRTVSSVLQ-SG
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IPR003006; Ig_MHC.
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CH2.
CH3.
CYTOPLASMIC (POTENTIAL).
E -> G (IN REF. 2).
E -> P (IN REF. 2).
P -> F (IN REF. 2).
CF7F264B50A41B95 CRC64;
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Pred. No. 5.1e
44; Mismatches
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RESULT 13
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ID GCAA_M
AC P01863
DT 21-JUL
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MEDLINE-81076554; PubMed=6777755;

Sikorav J.-L., Auffray C., Rougeon F.;

Sikorav J.-L., Auffray C., Rougeon F.;

Sikorav J.-L., Auffray C., Rougeon F.;

Balb/c gamma 2a heavy chain messenger RNA.";

Balb/c andds Res. 8:3143-3155(1980).
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15-SEP-2003 (Rel. 4
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21-JUL-1986
21-JUL-1986
15-SEP-2003
                              de Preval C., Fougereau M.;
"Determination of the primary structure of a mouse gamma immunoglobulin. Identification of the disulfide bridges."
Eur. J. Biochem. 30:452-462(1972)
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"The complete nucleotide sequence of mouse immunoglobin gamma 2a gene and evolution of heavy chain genes: further evidence for intervening sequence-mediated domain transfer.";
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                                                                                                                                                                      Bourgois A., Fougereau M., Rocca-Serra J.;
"Determination of the primary structure of a mouse IgG2a immunoglobulin:amino-acid sequence of the Fc fragment. Impl for the evolution of immunoglobulin structure and function. fur. J. Blochem. 43:423-435(1974).
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MEDLINE-81198976; PubMed-6262729;
Yamawaki-Kataoka Y., Miyata T., H
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MEDLINE=73056887; PubMed=4565406;
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family.";
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MEDLINE-81223894; PubMed-6787604;

Ollo R., Auffray C., Morchamps C., Rougeon F.;

"Comparison of mouse immunoglobulin gamma 2a and
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MEDLINE-74175517; PubMed-4831970;
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Brueggemann M., Delmastro-Galfre P., Waldmann H., 
"Sequence of a rat immunoglobulin gamma 2c heavy 
region cDNA: extensive homology to mouse gamma 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKRVEPKSCDKTHTCPP---CPAPEL
                          SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 474
                                                                                                                                                                                                                                                        QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS
                                                                                                                                                                                                                                                                                                                                    ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS
DSWMRGDIYTCSVVHEALHNHHTQKNLSRSPGK 329
                                                                                                                                          REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK
                                                                                                                                                                                                                          QLNGTFRVVSTLHIQHQDWMSGKEFKCKVNNKDLPSPIEKTISKPRGKARTPQVYTIPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLYTLSSSVTVPSSTWSSQTVTCSVAHPATKSNLIKRIEPR---RPKPRPPTDICSCDDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARTTAPSVYPLVPGCSGTSGSLVTLGCLVKGYFPEPVTVKWNSGALSSGVHTFPAVLQ-S
                                                                                                                REQMSKNKVSLTCMVTSFYPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR007110; Ig-like.
IPR003597; Ig_c1.
IPR003006; Ig_MHC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FΑB
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Rodentia;
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Pred. No. 2.5
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CH2.
CH3.
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INTERCHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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.5e-70;
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Query Match
Best Local
  Matches
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P01864;
21-JUL-1986
21-JUL-1986
15-SEP-2003
                                                                                         NON_TER
                                                                                                                                                                                                                                           PDB;
                                                                                                                                                                                                                                                                      PIR;
PDB;
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                               DOMAIN
DOMAIN
                                                                                                                                          SMART; SMO0407; IGC1; 2.
SMART; SMO0407; IGC1; 2.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
                                                                                                                                                                  InterPro; IPR007110; Ig-like InterPro; IPR003597; Ig_cl. InterPro; IPR003006; Ig_MHC. Pfam; PF00047; ig; 3.
SMART; SM00407; IGcl; 2.
                                                                                                                                                                                                                                   PDB;
                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                        -i- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF TH
FROM BALB/C MICE, AT 15% OF THE POSITIONS.
-i- SIMILARITY: Contains 3 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schreier P.H., Bothwell A.L.M., Mueller-Hill B., "Multiple differences between the nucleic acid se IgG2ah and IgG2ab alleles of the mouse."; proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation updat Ig gamma-2A chain C region secreted form (H Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-C57BL,
                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dognin M.J., Lauwereys M., Strosberg A.D.;
"Multiple amino acid substitutions between murine
chain Fc regions of Igla and Igla allotypic forms
Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=82037777; PubMed=6794027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                  3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=82037861; PubMed=6170065;
                                                                                                                              [mmunoglobulin domain; Immunoglobulin C
                                                                                                                                                                                                                                ; 1BOG; 23-MAR-99.
; 1HH6; 26-JAN-01.
; 1HH9; 12-JAN-01.
; 1HI6; 08-FEB-01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                ISOId-P01865-1; S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981 SUBCELLULAR LOCATION: Secreted (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=Membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name-Secreted;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Event=Alternative
                                                                                                                                                                                                                                                                                 A02153;
                                                                                                                                                                                                                                                                                            J00479; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Note=Probably the major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=P01864-1;
             Similarity
                                               126
234
335
  Conservative
                                                                                                                                                                                                                                                                                 G2MSAB
                                                                                                                 Repeat.
                                                  ΑA;
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                                                 98 I
225 I
330 I
36596 MW;
             44.8%;
61.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
  52;
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                                                              IG-LIKE
IG-LIKE
             Score 1126.5;
Pred. No. 2.96
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                                                   FA3382792CBB13C6 CRC64;
  Mismatches
                                                                 ω » :-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             335
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                                                                                                                             region; Alternative splicing;
              .9e-70;
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                         DB 1;
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RESULT

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